

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 17:12:40 ; Search time 183 Seconds
(without alignments)
170.693 Million cell updates/sec

Title: US-10-719-623A-16

Perfect score: 306

Sequence: 1 MFTLKSLLLFLGTLINLS.....EVEKRFPPVIGRLINGILGK 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	306	100.0	61	1	TEMG_RANTE
2	245	80.1	61	1	TEMH_RANTE
3	219.5	71.7	58	1	TEMH_RANTE
4	212	69.3	66	1	RLXN_RANCA
5	211.5	69.1	71	1	BRIE_RANES
6	189.5	61.9	65	1	GGNS_RANRU
7	184.5	60.3	69	1	BR1B_RANPI
8	155	50.7	331	2	Q7T2V5
9	148	48.4	80	1	GGN4_RANRU
10	145	47.4	71	1	RN2P_RANPI
11	144	47.1	62	1	PLR_RANPI
12	138.5	45.3	74	1	BR7A_RANTE
13	138.5	45.3	74	1	BR7B_RANTE
14	137.5	44.9	74	1	BR2F_RANES
15	136	44.4	62	1	RAYT_RANTE
16	133	44.1	70	1	RNZA_RANPI
17	133	43.5	66	2	Q800R3
18	120	39.2	84	1	ES1B_RANES
19	116.5	38.1	62	2	Q800F1
20	111	36.3	71	2	Q800S2
21	110	35.9	75	2	Q800R8
22	109	35.6	72	1	GALE_KASSE
23	109	35.6	77	1	DRG3_PHYBI
24	108	35.3	75	2	Q800R9
25	107	35.0	75	2	Q800S0
26	106.5	34.8	72	1	DM55_AGAAN
27	106	34.6	81	1	DRG1_PHYBI
28	106	34.6	201	1	DEM_PACDA
29	105.5	34.5	76	1	DMS4_PHYBI
30	105	34.3	72	1	DMS4_AGAAN
31	105	34.3	79	2	Q7T3K6

32	105	34.3	79	2	Q7T3K7
33	105	34.3	80	1	DMS2_PACDA
34	103.5	33.8	70	2	Q800R4
35	103.5	33.8	73	1	DMS2_AGAAN
36	103.5	33.8	76	2	Q7T3K8
37	103	33.7	71	2	Q800S1
38	103	33.7	75	1	DMS2_PACDA
39	103	33.7	77	1	DRG2_PHYBI
40	103	33.7	78	1	DMS1_PHYBI
41	103	33.7	80	1	DMS6_AGAAN
42	103	33.7	81	1	DMS2_PHYBI
43	102.5	33.5	72	1	DMS6_PHYBI
44	102.5	33.5	77	1	DERB_PHYBI
45	101.5	33.2	72	2	Q800R6

ALIGNMENTS

RESULT 1

ID	TEMG_RANTE	STANDARD;	PRT;	61 AA.
AC	P79875;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Temporin G precursor.			
OS	Rana temporaria (European common frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.			
OX	NCBI_TaxID=8407;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Skin;			
RA	MEDLINE=97175050; PubMed=9022710;			
RA	Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,			
RA	Barra D.;			
RT	Temporins, antimicrobial peptides from the European red frog Rana			
RT	temporaria.;			
RL	Eur. J. Biochem. 242:788-792(1996).			
CC	-!- FUNCTION: Has antibacterial activity against Gram-negative and			
CC	Gram-positive bacteria.			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- TISSUE SPECIFICITY: Skin.			
CC	-!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.			
CC	Brevinin subfamily.			

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DR	EMBL; Y09395; CAA70564.1; -
DR	InterPro; IPR004275; Brevenin.
DR	Pfam; PF03032; Brevinin; 1.
KW	Amidation; Amphibian defense peptide; Antibiotic; Signal.
FT	SIGNAL 1 22 Potential.
FT	PROPEP 23 44
FT	PEPTIDE 47 59 Temporin G.
FT	MOD_RES 59 59 Leucine amide (G-60 provides amide group).
FT	SEQUENCE 61 AA; 7171 MW; EDF5A8BC79DFD9F2 CRC64;

Query Match 100.0%; Score 306; DB 1; Length 61;
Best Local Similarity 100.0%; Pred. No. 3.8e-25;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFTLKSLLLFLGTLINLSLCEERDADEERDDLEERDVEVEKRFPPVIGRLINGILG 60

DB 1 MFTLKSLLLFLGTLINLSLCEERDADEERDDLEERDVEVEKRFPPVIGRLINGILG 60

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QY      61 K 61
Db      61 K 61

RESULT 2
TEMB_RANTE
ID      ID      TEMB_RANTE      STANDARD;      PRT;      61 AA.
AC      P79874;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Temporin B precursor.
OS      Rana temporaria (European common frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX      NCBI_TaxID=8407;
RN      [1]
RP      SEQUENCE FROM N.A., SEQUENCE OF 47-59, AND SYNTHESIS OF 47-59.
RC      TISSUE=Skin, and Skin secretion;
RX      MEDLINE=97175050; PubMed=9022710;
RA      Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA      Barra D.;
RT      "Temporins, antimicrobial peptides from the European red frog Rana
RT      temporaria.";
RL      Eur. J. Biochem. 242:788-792(1996).
CC      -|- FUNCTION: Has no antibacterial activity.
CC      -|- SUBCELLULAR LOCATION: Secreted.
CC      -|- TISSUE SPECIFICITY: Skin.
CC      -|- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC      Brevinin subfamily.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      use by non-profit institutions as long as its content is in no way
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; Y09393; CAA70562.1; -
DR      InterPro; IPR004275; Brevinin.
DR      Pfam; PF03032; Brevinin; 1.
KW      Amidation; Amphibian defense peptide; Direct protein sequencing;
KW      Signal.
FT      SIGNAL      1      22      Potential.
FT      PROPEP      23      44      Temporin H.
FT      PEPTIDE      47      56      Leucine amide (G-57 provides amide
FT      MOD_RES      56      56      group).
FT      SEQUENCE      58 AA; 6806 MW; 684ABC0451E5E81 CRC64;
SQ      -----
Query Match      71.7%; Score 219.5; DB 1; Length 58;
Best Local Similarity 73.8%; Pred. No. 5.8e-16;
Matches 45; Conservative 7; Mismatches 6; Indels 3; Gaps 1;

QY      1 MFTLKSLLLPFLGTINLSLCEERDADDERDVEVEKFFPVIGRLNGILG 60
      |||||
Db      1 MFTLKSLLLPFLGTINLSLCEERNABEERDEPDRDQVEKRLSP---NLKSLLG 57
      |||||

QY      61 K 61
Db      58 K 58

RESULT 4
RLXN_RANCA
ID      ID      RLXN_RANCA      STANDARD;      PRT;      66 AA.
AC      F39084;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Ranalexin precursor.
OS      Rana catesbeiana (Bull frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX      NCBI_TaxID=8400;
RN      [1]
RP      SEQUENCE FROM N.A., AND SEQUENCE OF 47-66.
RC      TISSUE=Skin, and Skin secretion;
RX      MEDLINE=94193792; PubMed=8144672;
RA      Clark D.P., Durell S., Maloy W.L., Zasloff M.;
RT      "Ranalexin. A novel antimicrobial peptide from bullfrog (Rana
RT      catesbeiana) skin, structurally related to the bacterial antibiotic,

```

RT polmyxin.";
 RL J. Biol. Chem. 269:10849-10855 (1994).
 RN [2]
 RP STRUCTURE BY NMR OF RANALEXIN.
 RX MEDLINE=98237592; PubMed=9578480;
 RA Aumelas A.; Chavanieu A., Roch P., Chiche L., Grassy G., Calas B.,
 RA "Solution structure of the antimicrobial peptide ranaalexin and a study
 RT of its interaction with perdeuterated dodecylphosphocholine
 RT micelles.";
 RL Eur. J. Biochem. 253:221-228 (1998).
 CC -!- FUNCTION: Potent microbicidal activity, active against S.aureus
 CC and E.coli. It acts as well as a membrane-disruptive agent at
 CC higher concentrations.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- DEVELOPMENTAL STAGE: Expression starts at metamorphosis and
 CC continues into adulthood.
 CC -!- SIMILARITY: Belongs to the frog skin active peptide (PSAP) family.
 CC Brevinin subfamily.
 CC
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 CC -----
 DR EMBL; S69903; AAB30394.1; -;
 DR PIR; A53744; A53744. Brevinin.
 DR InterPro; IPR004275; Brevinin.
 DR Pfam; PF03032; Brevinin; 1.
 KW Amphibian defense peptide; Antibiotic; Direct protein sequencing;
 KW Hemolysis; Signal.
 FT SIGNAL 1 20 Potential.
 FT PROPEP 21 44 Small acidic peptide.
 FT PEPTIDE 47 66 Ranaalexin.
 FT DISULFID 60 66
 SQ SEQUENCE 66 AA; 7615 MW; 096B8AD58A3C8513 CRC64;
 Query Match 69.3%; Score 212; DB 1; Length 66;
 Best Local Similarity 72.9%; Pred.No. 4.2e-15;
 Matches 43; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MFTLKSLLLFFLGITINISLCEERDADDEERDDLEERDVEVEKFFVIGRIILNGIL 59
 Db 1 MFTLKSLLLFFLGITINISLCEERDADDEERDDLEERDVEVEKFFVIGRIILNGIL 59
 RESULT 5
 ID BR1E RANES STANDARD; PRT; 71 AA.
 AC P32412;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Brevinin-1E precursor.
 OS Rana esculenta (Edible frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8401;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=94216303; PubMed=8163497;
 RA Simmaco M., Mignogna G., Barra D., Bossa F.;
 RT "Antimicrobial peptides from skin secretions of Rana esculenta.
 RT Molecular cloning of cDNAs encoding esculentin and brevinnins and
 RT isolation of new active peptides.";
 RL J. Biol. Chem. 269:11956-11961 (1994).
 RN [2]
 RP SEQUENCE OF 48-71, AND DISULFIDE BOND.

RC TISSUE=Skin secretion;
 RX MEDLINE=93285327; PubMed=8508915; DOI=10.1016/0014-5793(93)81384-C;
 RA Simmaco M., Mignogna G., Barra D., Bossa F.;
 RT "Novel antimicrobial peptides from skin secretion of the European frog
 RT Rana esculenta.";
 RL FEBS Lett. 324:159-161 (1993).
 CC -!- FUNCTION: Shows antibacterial activity against representative
 CC Gram-negative and Gram-positive bacterial species, and a very high
 CC hemolytic activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Skin.
 CC -!- SIMILARITY: Belongs to the frog skin active peptide (PSAP) family.
 CC Brevinin subfamily.
 CC
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 CC -----
 DR EMBL; X77831; CAA54842.1; -;
 DR PIR; C53578; C53578. Brevinin.
 DR InterPro; IPR004275; Brevinin.
 DR Pfam; PF03032; Brevinin; 1.
 KW Amphibian defense peptide; Antibiotic; Direct protein sequencing;
 KW Hemolysis; Signal.
 FT SIGNAL 1 22 Potential.
 FT PROPEP 23 45
 FT PEPTIDE 48 71 Brevinin-1E.
 FT DISULFID 65 71
 FT VARIANT 60 60 L -> F (in brevinnin-1E).
 SQ SEQUENCE 71 AA; 8267 MW; 10900AC2BC71BB73 CRC64;
 Query Match 69.1%; Score 211.5; DB 1; Length 71;
 Best Local Similarity 71.0%; Pred.No. 5.1e-15;
 Matches 44; Conservative 7; Mismatches 10; Indels 1; Gaps 1;
 QY 1 MFTLKSLLLFFLGITINISLCEERDADDEERDDLEERDVEVEKFFVIGRIILNGIL 59
 Db 1 MFTLKSLLLFFLGITINISLCEERDADDEERDDLEERDVEVEKFFVIGRIILNGIL 60
 QY 60 GK 61
 Db 61 PK 62
 RESULT 6
 ID GGN5_RANRU STANDARD; PRT; 65 AA.
 AC P80399; Q91329;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Gaegurin-5 precursor.
 GN Name=GGN5;
 OS Rana rugosa (Wrinkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Park J.M., Lee J.Y., Moon H.M., Lee B.J.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 42-65.
 RC TISSUE=Skin secretion;
 RX MEDLINE=95091844; PubMed=7999137;
 RA Park J.M., Jung J.-E., Lee B.J.;
 RT "Antimicrobial peptides from the skin of a Korean frog, Rana rugosa.";
 RL Biochem. Biophys. Res. Commun. 205:948-954 (1994).

CC -!- FUNCTION: Has a non-hemolytic activity. Has a broad spectrum of activity against both Gram-positive and Gram-negative bacteria, fungi and protozoa.

CC -!- SUBUNIT: Monomer.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Skin.

CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family. Brevinin subfamily.

CC -----

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CC -----

CC EMBL; U22393; AAA64412.1; -.

CC PIR; S59962; S59962.

CC InterPro; IPR004275; Brevenin.

CC Pfam; PF03032; Brevenin; 1.

CC Amphibian defense peptide; Antibiotic; Direct protein sequencing; Signal.

CC FT SIGNAL 1 22 Potential.

CC FT PROPEP 23 39

CC FT PEPTIDE 42 65 Gaegurin-5.

CC FT DISULFID 59 65 By similarity.

CC FT CONFLICT 58 58 F -> K (in Ref. 2).

CC SEQUENCE 65 AA; 7414 MW; 312480B867D4845 CRC64;

Query Match 61.9%; Score 189.5; DB 1; Length 65;

Best Local Similarity 67.8%; Pred. No. 1e-12; Indels 5; Gaps 1;

Matches 40; Conservative 8; Mismatches 6;

CC QY 1 MFTLKKSLLLPFLGTLINSLCEERDADEERDDLEERDVEVEKFRFPVIGRLNGIL 59

DB 1 MFTLKKSLLLPFLGTLINSLCEERDADEE-----EKRDVEVEKFRFGALFKVASKVL 54

RESULT 7

ID BR1B RANPI STANDARD; PRT; 69 AA.

AC Q8QF05; P82842;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Brevinin-1Pb precursor.

OS Rana pipiens (Northern leopard frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI_TaxID=8404;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Skin;

RA Farragher S.M., Bjourson A.J., Shaw C.;

RT "Cloning of Rana pipiens skin peptides."

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 46-69, FUNCTION, AND MASS SPECTROMETRY.

RC TISSUE=Skin secretion;

RX MEDLINE=20117700; PubMed=10651828;

RA Gorava J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E., Conlon J.M.;

RT "Peptides with antimicrobial activity from four different families isolated from the skins of the North American frogs Rana luteiventris, Rana berlandieri and Rana pipiens."

RL Eur. J. Biochem. 267:894-900(2000).

CC -!- FUNCTION: Antibacterial activity against Gram-positive bacterium S.aureus and Gram-negative bacterium E.coli. Has activity against C.albicans.

CC -!- SUBCELLULAR LOCATION: Secreted (Probable).

CC -!- TISSUE SPECIFICITY: Skin.

CC -!- MASS SPECTROMETRY: MW=2577.1; METHOD=Electrospray; RANGE=46-69;

CC NOTE=Ref.2.

CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family. Brevinin subfamily.

CC -----

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CC -----

CC EMBL; AJ427746; CAD20745.1; -.

CC InterPro; IPR004275; Brevenin.

CC Pfam; PF03032; Brevenin; 1.

CC Amphibian defense peptide; Antibiotic; Direct protein sequencing; Fungicide; Signal.

CC FT SIGNAL 1 20 Potential.

CC FT PROPEP 21 43

CC FT PEPTIDE 46 69 Brevinin-1Pb.

CC FT DISULFID 63 69 By similarity.

CC SEQUENCE 69 AA; 7929 MW; 31B16331997DC170 CRC64;

Query Match 60.3%; Score 184.5; DB 1; Length 69;

Best Local Similarity 65.6%; Pred. No. 3.7e-12; Indels 1; Gaps 1;

Matches 40; Conservative 6; Mismatches 14;

CC QY 1 MFTLKKSLLLPFLGTLINSLCEERDADEERDDLEERDVEVEKFRFPVIGRLNGIL 60

DB 1 MFTLKKSLLLPFLGTLINSLCEERDADEE-----EKRDVEVEKFRFGALFKVASKVL 54

QY 61 K 61

DB 60 K 60

RESULT 8

ID Q7T2V5 PRELIMINARY; PRT; 331 AA.

AC Q7T2V5;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Kininogen-1 precursor.

OS Rana schackeri.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI_TaxID=110116;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Skin;

RX MEDLINE=22830827; PubMed=12948838; DOI=10.1016/S0196-9781(03)00166-9; Li L., Bjourson A.J., He J., Cai G., Rao P., Shaw C.;

RT "Bradykinins and their cDNA from piebald odorless frog, Odorrana schackeri, skin."

RL Peptides 24:863-872(2003).

DR EMBL; AJ544062; CAD66432.1; -.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0042742; P:defense response to bacteria; IEA.

DR InterPro; IPR004275; Brevenin.

DR Pfam; PF03032; Brevenin; 1.

CC FT SIGNAL 1 24 Potential.

CC FT CHAIN 97 105 bradykinin.

CC FT CHAIN 141 149 bradykinin.

CC FT CHAIN 185 193 bradykinin.

CC FT CHAIN 229 237 bradykinin.

CC FT CHAIN 273 281 bradykinin.

CC FT CHAIN 317 325 bradykinin.

CC FT CHAIN 53 61 bradykinin.

CC SEQUENCE 331 AA; 37680 MW; D7DF35CB3A45066D CRC64;

Query Match 50.7%; Score 155; DB 2; Length 331;

Query Match 48.4%; Score 148; DB 1; Length 80;
Best Local Similarity 49.3%; Pred. No. 3.3e-08;
Matches 34; Conservative 11; Mismatches 14; Indels 10; Gaps 2;

QY	1	MFTLKSLLLLFFLGTINLSICEERDADAERDDL EERDV.-----EVEKEFPFVTRIL	55
Db	1	MFTMKSLLLLFFLGTISLSICEERSADEDGGTEEEVCRGILDTLKQFAKGVGKOL	60

Qy 56 -----NGIL 59

db 61 VKGAAGVT. 69

RESULT 10

RN2F_RANPI	ID_RN2P_RANPI	STANDARD;	PRT;	71 AA.
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AC Q8QFEQ4; P82847;
DT 10-OCT-2003 (Re) 42. Created)

DT	10-OCT-2003 (Rel. 42, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last sequence update)

DE Ranatuerin-2P precursor.

OS *Rana pipiens* (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OY NCBI TaxID-8404.

RN [1] -

RC TISSUE=Skin;

RT "Cloning of *Rana pipiens* skin peptides."; Farragher S.M., Bjourson A.J., Shaw C.; RA

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
PN [2]

RP SEQUENCE OF 45-71, FUNCTION, AND MASS SPECTROMETRY.

RX MEDLINE=20117700; PubMed=10651828;

RA Goraya J., Wang Y., Li Z., O'Flaherty M., Knoop F.C., Platz J.E.,
RA Conlon J.M.;

RT "Peptides with antimicrobial activity from four different families
PT isolated from the skins of the North American frog *Rana luteiventris*

RT Rana berlandieri and Rana pipiens." ;

CC -!- FUNCTION: Antibacterial activity against Gram-positive bacterium

CC S.aureus and Gram-negative bacterium E.coli. Has activity against C.albicans.

CC -|- SUBCELLULAR LOCATION: secreted.
CC -|- TISSUE SPECIFICITY: skin

```
CC -!- MASS SPECTROMETRY: MW=3000.1; METHOD=Electrospray; RANGE=45-71;
```

CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.

cc Brevinin subfamily.

cc

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DR InterPro; IPR004275; Brevenin.

DR Pfam; PF03032; Brevenin; 1.
KW Amphibian defense peptide; Antibiotic; Direct protein sequencing;

FT	Fungicide; Signal.	Potential
1	20	

FT	PROPEP	21	44
CE	DEPTOC	45	71

FT	DISULFID	66	71	By similarity.
----	----------	----	----	----------------

SQ SEQUENCE /I AA; /94I MW; C8/IC4/FC2/FFDEF CRC64;

Query Match	47.4%	Score 145; DB 1; Length 71;
Best [local] Similarity	50.0%	Pred. No. 6.1e-08;

Matches 30; Conservative 11; Mismatches 17; Indels 2; Gaps 1;

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CC -----
DR EMBL; AJ414584; CAC93861.1; -
DR GO; GO:0005576; C:extracellular; IDA.
DR GO; GO:0005083; P:defense response to fungi; IDA.
DR GO; GO:0005083; P:defense response to Gram-positive bacteria; IDA.
DR InterPro; IPR004275; Brevenin.
DR Pfam; PF03032; Brevenin; 1.
KW Amidation; Amphibian defense peptide; Antibiotic;
KW Cleavage on pair of basic residues; Direct protein sequencing;
KW Fungicide; Hemolysis; Inflammatory response; Mast cell degranulation;
KW Signal.
FT SIGNAL 1 20 Potential.
FT PROPEP 21 41 Peptide leucine arginine.
FT PEPTIDE 44 61
FT DISULFID 48 58
FT MOD_RES 61 61 Arginine amide (G-62 provides amide
FT group).
SQ SEQUENCE 62 AA; 7113 MW; C8F7F5849A01A1C CRC64;
Query Match 47.1%; Score 144; DB 1; Length 62;
Best Local Similarity 52.6%; Pred. No. 6.8e-08;
Matches 30; Conservative 11; Mismatches 6; Indels 10; Gaps 1;
QY 1 MFTLKKSLLLFLGLTINLSCEERDADDEERDDLEERDVEVERKFFPVIGRLNGIAG 57
DB 1 MFTLKKSLLLFLGLTINLSCEERDADDEERDDLEERDVEVERKFFPVIGRLNGIAG 47
RESULT 12
ID BRTA_RANTE STANDARD; PRT; 74 AA.
AC P82268;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Brevenin-2Ta precursor.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Simmaco M., Miele R., Mangoni M.L., Barra D.;
RT "A cDNA clone encoding brevenin 2Ta from Rana temporaria.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Shows antibacterial activity against representative
CC Gram-negative and Gram-positive bacterial species (by similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Brevenin subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ251567; CAB61442.1; -
DR InterPro; IPR004275; Brevenin.
DR Pfam; PF03032; Brevenin; 1.
KW Amphibian defense peptide; Antibiotic; Hemolysis; Signal.
FT SIGNAL 1 22
QY 1 MFTLKKSLLLFLGLTINLSCEERDADDEERDDLEERDVEVERKFFPVIGRLNGIAG 60
DB 1 MFTLKKSLLLFLGLTINLSCEERDADDEERDDLEERDVEVERKFFPVIGRLNGIAG 58
RESULT 11
ID FLR_RANPI STANDARD; PRT; 62 AA.
AC Q90MP7; P82110;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Peptide leucine arginine precursor (pLR).
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Farragher S., Bjourson A.J., McClean S., Orr D.F., Shaw C.;
RT "Cloning of cDNAs encoding defensive skin secretion peptides from the
RT Northern leopard frog (Rana pipiens).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE OF 44-61, FUNCTION, MASS SPECTROMETRY, DISULFIDE BOND,
RN CIRCULAR DICHROISM ANALYSIS, SYNTHESIS, AND 3D-STRUCTURE MODELING.
RN TISSUE=Skin secretion;
RX MEDLINE=21167822; PubMed=11099505; DOI=10.1074/jbc.M009680200;
RA Salmon A.L., Cross L.J.M., Irvine A.E., Lappin T.R.J., Dache M.,
RA Krause G., Canning P., Thim L., Beyeremann M., Rothmund S.,
RA Bienert M., Shaw C.;
RT "Peptide leucine arginine, a potent immunomodulatory peptide, isolated
RT and structurally characterized from the skin of the Northern Leopard
RT frog, Rana pipiens.";
RL J. Biol. Chem. 276:10145-10152(2001).
RN [3]
RN FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=98338373; PubMed=9673585;
RA Boyer M., van Den Berg H.W., Shaw C., Lynch M., Johnston P.;
RT "Breast cancer cell lines express specific binding sites for pLR, a
RT novel anti-proliferative peptide from frog skin venom.";
RL Br. J. Cancer 78:41-41(1998).
RN [4]
RN FUNCTION.
RX PubMed=14636071; DOI=10.1021/bi0345211;
RA Mangoni M.L., Papo N., Mignogna G., Andreu D., Shai Y., Barra D.,
RA Simmaco M.;
RT "Kanamycin, a new family of short cyclic antimicrobial peptides:
RT biological function, mode of action and parameters involved in target
RT specificity.";
RL Biochemistry 42:14023-14035(2003).
CC -!- FUNCTION: Mast cell degranulating peptide. Antiproliferative
CC activity against human breast and ovarian tumor cell lines in
CC vitro. Inhibits granulopoiesis in rat in vitro. Causes histamine
CC release from rat peritoneal mast cells in vitro. Has antibacterial
CC activity against Gram-positive bacteria B.megaterium Bm1,
CC S.lentus and M.luteus, and antifungal activity against
CC C.tropicalis, C.guillier-mondii and P.nicotianae spores. Has
CC hemolytic activity. The mature peptide inserts into the
CC hydrophobic core of the bacterial cell membrane and increases
CC permeability without disrupting membrane integrity. Probably binds
CC to the outer membrane surface before aggregating to form
CC transmembrane pores.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=2136; METHOD=Plasma desorption; RANGE=44-61;
CC NOTE=Ref.2.
CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Brevenin subfamily.
CC -----

```
FT PROPEP      23 39          Brevinin-2Ta.
FT PEPTIDE     42 74          By similarity.
FT DISULFID    68 74
SQ SEQUENCE    74 AA; 8162 MW; 5580FDF790B78F75 CRC64;

Query Match
Best Local Similarity 45.3%; Score 138.5; DB 1; Length 74;
Matches 30; Conservative 6; Mismatches 5; Indels 5; Gaps 1;

QY 1 MFTLKSLLLFFLGLTINSLCEERDADDERDDLEERDVEVEKR 46
Db 1 MFTMKKSLLLFFLGLTISLCOERNADDDGEMTEE-----EKR 41

RESULT 13
ID BR2F_RANES STANDARD; PRT; 74 AA.
AC P82269;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Brevinin-2TB precursor.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 42-74.
TISSUE=Skin, and skin secretion;
RX MEDLINE=99266278; PubMed=10333736;
RX DOI=10.1002/(SICI)1097-0282(1998)47:6<435::AID-BIP33.3.CO;2-#;
RA Simmaco M., Mignogna G., Barra D.,
RT "Antimicrobial peptides from amphibian skin: what do they tell us?";
RL Biopolymers 47:435-450(1998).
CC Gram-negative and Gram-positive activity against representative
CC -!- FUNCTION: Shows antibacterial activity against representative
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Brevinin subfamily.
CC
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CC
CC EMBL; AJ251566; CAB61445.1; -.
CC InterPro; IPR004275; Brevinin.
CC Pfam; PF03032; Brevinin; 1.
CC KW Amphibian defense peptide; Antibiotic; Direct protein sequencing;
CC Hemolysis; Signal.
CC SIGNAL 1 22 Potential.
CC PROPEP 23 39 Brevinin-2Tb.
CC PEPTIDE 42 74 By similarity.
CC DISULFID 68 74
CC SEQUENCE 74 AA; 8193 MW; 5B26718D62B79387 CRC64;

Query Match
Best Local Similarity 45.3%; Score 138.5; DB 1; Length 74;
Matches 30; Conservative 6; Mismatches 5; Indels 5; Gaps 1;

QY 1 MFTLKSLLLFFLGLTINSLCEERDADDERDDLEERDVEVEKR 46
Db 1 MFTMKKSLLLFFLGLTISLCOERNADDDGEMTEE-----EKR 41

RESULT 14
BR2F_RANES STANDARD; PRT; 74 AA.
ID BR2F_RANES
AC P40872;

DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Brevinin-2EF precursor.
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8401;
RN [1]
SEQUENCE FROM N.A.
TISSUE=Skin;
RX MEDLINE=94216303; PubMed=8163497;
RA Simmaco M., Mignogna G., Barra D., Bessa F.,
RT "Antimicrobial peptides from skin secretions of Rana esculenta.
RT Molecular cloning of cDNAs encoding esculentin and brevinins and
RT Isolation of new active peptides.";
RL J. Biol. Chem. 269:11956-11961(1994).
CC -!- FUNCTION: Shows antibacterial activity against representative
CC Gram-negative and Gram-positive bacterial species, and hemolytic
CC activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Brevinin subfamily.
CC
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CC
CC EMBL; X77832; CAAS4843.1; -.
CC PIR; B53578; B53578.
CC InterPro; IPR004275; Brevinin.
CC Pfam; PF03032; Brevinin; 1.
CC KW Amphibian defense peptide; Antibiotic; Hemolysis; Signal.
CC SIGNAL 1 22 Potential.
CC PROPEP 23 39 Brevinin-2EF.
CC PEPTIDE 42 74 By similarity.
CC DISULFID 68 74
CC SEQUENCE 74 AA; 8134 MW; 48044D3F01E6D78D CRC64;

Query Match
Best Local Similarity 63.0%; Score 137.5; DB 1; Length 74;
Matches 29; Conservative 8; Mismatches 4; Indels 5; Gaps 1;

QY 1 MFTLKSLLLFFLGLTINSLCEERDADDERDDLEERDVEVEKR 46
Db 1 MFTMKKSLLLFFLGLTISLCOERNADDDGEMTEE-----EKR 41

RESULT 15
ID RAYT_RANTE STANDARD; PRT; 62 AA.
AC P83719;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ranacyclin T precursor.
GN Name=RNCT;
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8407;
RN [1]
SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin;
RX PubMed=14636071; DOI=10.1021/bi034521l;
RA Mangoni M.L., Papo N., Mignogna G., Andreu D., Shai Y., Barra D.,
RA Simmaco M.,
RT "Ranacyclins, a new family of short cyclic antimicrobial peptides:
```


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OM protein - protein search, using sw model

Run on: March 30, 2005, 17:20:45 ; Search time 43 Seconds
(without alignments)
136.494 Million cell updates/sec

Title: US-10-719-623A-16
Perfect score: 306
Sequence: 1 MFTLKSLLLFLGLTINLS.....EVEKRFPPVIGRLNGILCK 61
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	212	69.3	66	1 A53744	ranalexin precursor
2	211.5	69.1	71	2 C53578	brevinin-18c precursor
3	189.5	61.9	65	2 S59962	antimicrobial peptide
4	148	48.4	80	2 S59961	antimicrobial peptide
5	137.5	44.9	74	2 B53578	brevinin-28f precursor
6	120	39.2	84	2 A53578	esculentin-1b precursor
7	103	33.7	78	2 B54897	dermaseptin b1 precursor
8	103	33.7	81	1 JN0462	adenoregulin precursor
9	99.5	32.5	74	2 T10456	dermaseptin b3 precursor
10	99.5	32.5	198	2 B27784	dermorphin precursor
11	98	32.0	197	1 A27784	dermorphin precursor
12	96	31.4	227	2 A35514	[D-Ala(2)] deitorp
13	70.5	23.0	645	1 A23723	protein disulfide
14	70	22.9	429	2 F71896	hypothetical protein
15	69.5	22.7	213	2 G69850	hypothetical protein
16	69	22.5	152	2 G85090	hypothetical protein
17	68	22.2	313	2 B96892	hypothetical protein
18	66	21.6	436	2 B23364	procaerulein precursor
19	66	21.6	429	2 E64617	hypothetical protein
20	65	21.2	185	2 G70425	hypothetical protein
21	65	21.2	188	2 A23364	caerulein precursor
22	64.5	21.1	361	2 A96261	hypothetical protein
23	64.5	21.1	361	2 AH3023	efflux protein, [lm
24	64	20.9	833	2 T22139	hypothetical protein
25	64	20.9	1684	2 T02367	hypothetical protein
26	63	20.6	490	2 A86265	Cytochrome P450 71
27	62.5	20.4	763	2 A49321	amyloid beta (A4)
28	62	20.3	84	2 AG3788	hypothetical protein
29	62	20.3	201	2 A86363	protein F26H11.1 [

30	62	20.3	241	2 T51964	probable ubiquitin
31	62	20.3	244	2 T21434	hypothetical protein
32	62	20.3	316	2 G95513	hypothetical protein
33	62	20.3	1110	2 I51116	NF-180 - sea lamp
34	61.5	20.1	630	2 S29796	hypothetical protein
35	61.5	20.1	721	2 S29795	hypothetical protein
36	61	19.9	1198	2 D96723	hypothetical protein
37	60.5	19.8	172	2 G70234	conserved hypochet
38	60	19.6	81	2 T48398	hypothetical protein
39	60	19.6	150	2 F75070	hypothetical protein
40	60	19.6	289	2 D69152	hypothetical protein
41	60	19.6	678	2 A54514	glutamic acid-rich
42	60	19.6	1430	2 T21910	hypothetical protein
43	59.5	19.4	186	2 A72363	3-isopropylmalate
44	59.5	19.4	232	2 F84798	hypothetical protein
45	59.5	19.4	296	2 A41730	nucleophosmin NO38

ALIGNMENTS

RESULT 1

A53744
ranalexin precursor - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A53744
J:Clark, D.P.; Durell, S.; Maloy, W.L.; Zasloff, M.
J: Biol. Chem. 269, 10849-10855, 1994
A:Title: Ranalexin. A novel antimicrobial peptide from bullfrog (Rana catesbeiana) skin.
A:Reference number: A53744, MUID:94193792; PMID:8144672
A:Accession: A53744
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-66 <CLA>
A:Cross-references: UNIPROT:P39084; GB:S69903; NID:G546211; PIDN:AAB30394.1; PID:G546212
C:Superfamily: ranalexin precursor; dermorphin precursor amino-terminal homology
C:Keywords: disulfide bond; skin
F:1-46/Domain: dermorphin precursor amino-terminal homology <DER>
F:47-66/Product: ranalexin #status experimental <MAT>
F:60-66/Disulfide bonds: #status experimental

Query Match 69.3%; Score 212; DB 1; Length 66;
Best Local Similarity 72.9%; Pred. No. 1.6e-16;
Matches 43; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

QY 1 MFTLKSLLLFLGLTINLSLCEERDADDERDDLEERDVEVERKFFPVIGRLNGIL 59
DB 1 MFTLKSLLLFLGLTINLSLCEERDADDERDDLEERDVEVERKFFPVIGRLNGIL 59

RESULT 2

C53578
brevinin-18c precursor - edible frog
N:Alternate names: antimicrobial peptide brevinin 1B
C:Species: Rana esculenta (edible frog)
C>Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C:Accession: C53578; S33729
R:Simmaco, M.; Mignogna, G.; Barra, D.; Bossa, F.
J: Biol. Chem. 269, 11956-11961, 1994
A:Title: Antimicrobial peptides from skin secretions of Rana esculenta. Molecular cloning
A:Reference number: A53578; MUID:94216303; PMID:8163497
A:Accession: C53578
A:Molecule type: mRNA
A:Residues: 1-71 <STM>
A:Cross-references: UNIPROT:P32412; GB:X77831; NID:G488372; PIDN:CAA54842.1; PID:G140579;
R:Simmaco, M.; Mignogna, G.; Barra, D.; Bossa, F.
FEBS Lett. 324, 159-161, 1993
A:Title: Novel antimicrobial peptides from skin secretion of the European frog Rana escul
A:Reference number: S33729; MUID:93285327; PMID:8508915
A:Accession: S33729
A:Molecule type: protein
A:Residues: 48-71 <SIW>

A;Experimental source: skin

C;Function: has antimicrobial and hemolytic activity
 C;Superfamily: ranalexin precursor; dermorphin precursor amino-terminal homology
 C;Keywords: antibacterial; disulfide bond; hemolysis; skin
 F;1-47/Domain: dermorphin precursor amino-terminal homology <DER>
 F;1-22/Domain: signal sequence #status predicted <SIG>
 F;23-47/Domain: propeptide #status predicted <PRO>
 F;48-71/Product: brevinin-1Ec #status experimental <MAT>
 F;65-71/Disulfide bonds: #status predicted

Query Match 69.1%; Score 211.5; DB 2; Length 71;
 Best Local Similarity 71.0%; Pred. No. 1.9e-16;
 Matches 44; Conservative 7; Mismatches 10; Indels 1; Gaps 1;

QY 1 MFTLKSLLLPFLGTINLSLCEERDAD-ERRDDLEERDVEVEKRPFPVIGRIINGIL 59
 DB 1 MFTLKSLLLPFLGTINLSLCEERDADDEERRDNDPDESEVEVEKRFUPLLAGLAANFL 60

QY 60 GK 61

DB 61 PK 62

RESULT 3
 S59962
 antimicrobial peptide gaegurin 5 precursor - Korean frog

C;Species: Rana rugosa (Korean frog)
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C;Accession: S59962; PC2304

R;Park, J.M.; Lee, J.Y.; Moon, H.M.; Lee, B.J.

Biochim. Biophys. Acta 1264, 23-25, 1995

A;Title: Molecular cloning of cDNAs encoding precursors of frog skin antimicrobial peptide

A;Reference number: S59961; MUID:96038814; PMID:7578251

A;Accession: S59962

A;Molecule type: mRNA

A;Residues: 1-65 <PAR>

A;Cross-references: UNIPROT:P80399; EMBL:U22393; NID:g733137; PIDN:AAA64412.1; PID:g7331

A;Experimental source: skin

R;Park, J.M.; Jung, J.E.; Lee, B.J.

Biochem. Biophys. Res. Commun. 205, 948-954, 1994

A;Title: Antimicrobial peptides from the skin of a Korean frog, Rana rugosa.

A;Reference number: PC2300; MUID:95091844; PMID:7999137

A;Accession: PC2304

A;Molecule type: protein

A;Residues: 42-57, 'K', 59-65 <PAW>

A;Experimental source: skin

C;Comment: This peptide has antimicrobial activity.

C;Superfamily: ranalexin precursor; dermorphin precursor amino-terminal homology

C;Keywords: antibacterial; antibiotic; antifungal; disulfide bond; skin

F;1-41/Domain: dermorphin precursor amino-terminal homology <DER>

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-41/Domain: propeptide #status predicted <PRO>

F;44-65/Product: antimicrobial peptide gaegurin 5 #status experimental <MAT>

F;59-65/Region: rana box motif

Query Match 61.9%; Score 189.5; DB 2; Length 65;

Best Local Similarity 67.8%; Pred. No. 4.6e-14;

Matches 40; Conservative 8; Mismatches 6; Indels 5; Gaps 1;

QY 1 MFTLKSLLLPFLGTINLSLCEERDADDEERRDDLEERDVEVEKRPFPVIGRIINGIL 59
 DB 1 MFTLKSLLLPFLGTINLSLCEERNADEE-----EKRDVEVEKRFGLNALFKVASKVL 54

RESULT 4

S59961

antimicrobial peptide gaegurin 4 precursor - Korean frog

C;Species: Rana rugosa (Korean frog)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S59961; PC2303

R;Park, J.M.; Lee, J.Y.; Moon, H.M.; Lee, B.J.

Biochim. Biophys. Acta 1264, 23-25, 1995

A;Title: Molecular cloning of cDNAs encoding precursors of frog skin antimicrobial peptide

A;Reference number: S59961; MUID:96038814; PMID:7578251

A;Accession: S59961

A;Molecule type: mRNA

A;Residues: 1-80 <PAR>

A;Cross-references: UNIPROT:P80398; EMBL:U22392; NID:g733135; PIDN:AAA64411.1; PID:g7331

R;Park, J.M.; Jung, J.E.; Lee, B.J.

Biochem. Biophys. Res. Commun. 205, 948-954, 1994

A;Title: Antimicrobial peptides from the skin of a Korean frog, Rana rugosa.

A;Reference number: PC2300; MUID:95091844; PMID:7999137

A;Accession: PC2303

A;Molecule type: protein

A;Residues: 44-77, 'L', 79-80 <PAW>

A;Experimental source: skin

C;Comment: This peptide has antimicrobial activity.

C;Superfamily: ranalexin precursor; dermorphin precursor amino-terminal homology

C;Keywords: antibacterial; antibiotic; antifungal; disulfide bond; skin

F;1-43/Domain: dermorphin precursor amino-terminal homology <DER>

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-43/Domain: propeptide #status predicted <PRO>

F;44-80/Product: antimicrobial peptide gaegurin 4 #status experimental <MAT>

F;74-80/Region: rana box motif

Query Match 48.4%; Score 148; DB 2; Length 80;

Best Local Similarity 49.3%; Pred. No. 2.1e-09;

Matches 34; Conservative 11; Mismatches 14; Indels 10; Gaps 2;

QY 1 MFTLKSLLLPFLGTINLSLCEERDADDEERRDDLEERDV-----EVEKRPFPVIGRIIL 55
 DB 1 MFTMKSLLLPFLGTISLSLCEERSADEDDGGWTEEVKRGILDTLKQPAKGVGKOL 60

QY 56 -----NGIL 59

DB 61 VKGAAGQVIL 69

RESULT 5

B53578

brevinin-2Ef precursor - edible frog

C;Species: Rana esculenta (edible frog)

C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004

C;Accession: B53578

R;Simmaco, M.; Mignogna, G.; Barra, D.; Bossa, F.

J. Biol. Chem. 269, 11956-11961, 1994

A;Title: Antimicrobial peptides from skin secretions of Rana esculenta. Molecular cloning

A;Reference number: A53578; MUID:94216303; PMID:8163497

A;Accession: B53578

A;Molecule type: mRNA

A;Residues: 1-74 <SIM>

A;Cross-references: UNIPROT:P40842; GB:X77832; NID:G488373; PIDN:CAA54843.1; PID:g140579f

C;Superfamily: ranalexin precursor; dermorphin precursor amino-terminal homology

C;Keywords: antibacterial; disulfide bond; skin

F;1-41/Domain: dermorphin precursor amino-terminal homology <DER>

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-41/Domain: propeptide #status predicted <PRO>

F;42-74/Product: brevinin-2Ef #status predicted <MAT>

F;68-74/Disulfide bonds: #status predicted

Query Match 44.9%; Score 137.5; DB 2; Length 74;

Best Local Similarity 63.0%; Pred. No. 2.7e-08;

Matches 29; Conservative 8; Mismatches 4; Indels 5; Gaps 1;

QY 1 MFTLKSLLLPFLGTINLSLCEERDADDEERRDDLEERDVEVEK 46

DB 1 MFTMKSLLLPFLGTISLSLCEERNADDDDGEMTEE-----EKR 41

RESULT 6

A53578

esculentin-lb precursor - edible frog

C;Species: Rana esculenta (edible frog)

C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004

C;Accession: A53578

A:Molecule type: mRNA
A:Residues: 1-81 <AMT>
A/Cross-references: UNIPROT:P31107; EMBL:X70278; NID:g395931; PIDN:CAA49763.1; PID:g395935
A:Experimental source: skin
A/Note: the authors translated the codon AAA for residue 26 as Leu
R:Amiche, M.; Ducancel, F.; Mox, A.; Boulain, J.C.; Menez, A.; Nicolas, P.
J. Biol. Chem. 269, 17847-17852, 1994
A/Title: Precursors of vertebrate peptide antibiotics dermaseptin b and adenoregulin hav:
A/Reference number: A54897; MUID:94299491; PMID:8074751
A/Accession: A54897
A:Molecule type: mRNA
A:Residues: 1-81 <AMZ>
A/Cross-references: GB:X70278; NID:g395931; PIDN:CAA49763.1; PID:g395932
R:Daly, J.W.; Caceres, J.; Moni, R.W.; Gusovsky, F.; Moos Jr., M.; Seamon, K.B.; Milton,
proc. Natl. Acad. Sci. U.S.A. 89, 10960-10963, 1992
A/Title: Frog secretions and hunting magic in the upper Amazon: identification of a pept
A/Reference number: A44171; MUID:93066363; PMID:1438301
A/Accession: A44171
A:Molecule type: protein
A:Residues: 46-78 <DAL>
C:Superfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology
C/Keywords: antibiotic; antifungal; skin
F:1-45/Domain: dermorphin precursor amino-terminal homology <DER>
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-45/Domain: propeptide #status predicted <PRO>
F:46-78/Product: adenoregulin #status experimental <MAT>
Query Match 33.7%; Score 103; DB 1; Length 81;
Best Local Similarity 47.7%; Pred. No. 0.00018;
Matches 21; Conservative 12; Mismatches 9; Indels 2; Gaps 1;
QY 1 MFTLKSLLLFLFGTINLSICEER--DADERRDDLEERDVE 42
DB 1 MAFELKSLFVLFLGLVSLSCIEKEKRENEDEEDDEQSEMK 44
RESULT 9
T10456
dermaseptine B3 precursor - two-colored leaf frog
C:Species: Phyllomedusa bicolor (two-colored leaf frog)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T10456
R:Charpentier, S.; Amiche, M.; Meater, J.; Vouille, V.; Le Caer, J.P.; Niicolas, P.; Dell
J. Biol. Chem. 273, 14690-14697, 1998
A/Title: Structure, synthesis, and molecular cloning of dermaseptins B, a family of skin
A/Reference number: Z17027; MUID:98278974; PMID:9614066
A/Accession: T10456
A/Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-74 <CHA>
A/Cross-references: UNIPROT:P81485; EMBL:Y16564; NID:g3256036; PIDN:CAA76288.1; PID:g3256
C:Superfamily: dermaseptin precursor; dermorphin precursor amino-terminal homology
F:1-22/Domain: signal sequence #status predicted <SIG>
F:23-74/Product: dermaseptine B3 #status predicted <MAT>
Query Match 32.58%; Score 99.5; DB 2; Length 74;
Best Local Similarity 45.8%; Pred. No. 0.00041;
Matches 22; Conservative 13; Mismatches 8; Indels 5; Gaps 2;
QY 1 MFTLKSLLLFLFGTINLSICEER--DADERRDDLEERDVEVEKR 46
DB 1 MAFELKSLFVLFLGLVSLSCIEKEKRENEEKQEDDEQSE--EKR 45
RESULT 10
B27784
dermorphin precursor 2 - Sauvage's leaf frog (fragment)
N:Contains: dermorphin
C:Species: Phyllomedusa sauvaigi (Sauvage's leaf frog)
C/Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C/Accession: B27784
R:Richter, K.; Egger, R.; Kreil, G.

Science 238, 200-202, 1987
 A:Title: D-alanine in the frog skin peptide dermatophin is derived from L-alanine in the
 A:Reference number: A94297; MUID:88017999; PMID:3659910
 A:Accession: B27784
 A:Molecule type: mRNA
 A:Residues: 1-198 <RIC>
 A:Cross-references: UNIPROT:P05421; GB:M18030; NID:G213542; PID:AAA49452.1; PID:G213543
 C:Comment: The precursor contains tandem repeats separated by paired basic residues as in
 vity.
 C:Superfamily: dermatophin precursor; dermatophin precursor amino-terminal homology
 C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide; skin; tandem repeat
 F:1-47/Domain: dermatophin precursor amino-terminal homology <DER>
 F:56-62/Domain: dermatophin repeat <RPT1>
 F:48-54/Product: dermatophin #status experimental <DER1>
 F:63-89/Domain: dermatophin repeat <RPT2>
 F:83-99/Product: dermatophin #status experimental <DER2>
 F:99-133/Domain: dermatophin repeat <RPT3>
 F:118-124/Product: dermatophin #status experimental <DER3>
 F:134-168/Domain: dermatophin repeat <RPT4>
 F:153-159/Product: dermatophin #status experimental <DER4>
 F:169-198/Domain: dermatophin repeat (partial) <RPT5>
 F:188-194/Product: dermatophin #status experimental <DER5>
 F:54/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly
 F:89/Modified site: D-alanine (Ala) #status experimental
 F:99/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly
 F:119/Modified site: D-alanine (Ala) #status experimental
 F:124/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly
 F:154/Modified site: D-alanine (Ala) #status experimental
 F:159/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly
 F:189/Modified site: D-alanine (Ala) #status experimental
 F:194/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly
 Query Match 32.5%; Score 99.5; DB 2; Length 198;
 Best Local Similarity 45.8%; Pred. No. 0.001;
 Matches 22; Conservative 10; Mismatches 15; Indels 1; Gaps 1;
 QY 1 MFTLKSLLLFLPLGTINSLCEERDADDERDDLEERDVEVE-KRF 47
 DB 1 MSFLKSLLLFLPLGLVSLVCKEERTEENENHEEGSEMRY 48
 RESULT 11
 A27784
 N:Contains: dermatophin precursor 1 - Sauvage's leaf frog
 C:Species: Phyllomedusa sauvagei (Sauvage's leaf frog)
 C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C:Accession: A27784; A60595
 R:Richter, K.; Egger, R.; Kreil, G.
 Science 238, 200-202, 1987
 A:Title: D-alanine in the frog skin peptide dermatophin is derived from L-alanine in the
 A:Reference number: A94297; MUID:88017999; PMID:3659910
 A:Accession: A27784
 A:Molecule type: mRNA
 A:Residues: 1-197 <RIC>
 A:Cross-references: UNIPROT:P05422; GB:M18031; NID:G213544; PID:AAA49453.1; PID:G213545
 Eur. J. Pharmacol. 162, 123-128, 1989
 A:Title: Dermatophin, a novel amphibian skin peptide with high selectivity and affinity f
 A:Reference number: A60595; MUID:89251774; PMID:2542051
 A:Accession: A60595
 A:Molecule type: protein
 A:Residues: 48-54 <KRE>
 C:Comment: The precursor contains tandem repeats separated by paired basic residues as i
 vity.
 C:Superfamily: dermatophin precursor; dermatophin precursor amino-terminal homology
 C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide; skin; tandem repeat
 F:1-47/Domain: dermatophin precursor amino-terminal homology <DER1>
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:26-60/Domain: dermatophin repeat <RPT1>
 F:48-54/Product: dermatophin #status experimental <DLT>
 F:61-95/Domain: dermatophin repeat <RPT2>
 F:69-114/Domain: dermatophin precursor amino-terminal homology <DER2>

F:80-86/Product: dermatophin #status experimental <MAT1>
 F:96-130/Domain: dermatophin repeat <RPT3>
 F:115-121/Product: dermatophin #status experimental <MAT2>
 F:131-165/Domain: dermatophin repeat <RPT4>
 F:150-156/Product: dermatophin #status experimental <MAT3>
 F:166-197/Domain: dermatophin repeat <RPT5>
 F:185-191/Product: dermatophin #status experimental <MAT4>
 F:49/Modified site: D-methionine (Met) #status experimental
 F:54/Modified site: amidated carboxyl end (Asp) (amide in mature form from following gly
 F:81/Modified site: D-alanine (Ala) #status experimental
 F:86/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly
 F:116/Modified site: D-alanine (Ala) #status experimental
 F:121/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly
 F:151/Modified site: D-alanine (Ala) #status experimental
 F:156/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly
 F:186/Modified site: D-alanine (Ala) #status experimental
 F:191/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly
 Query Match 32.0%; Score 98; DB 1; Length 197;
 Best Local Similarity 44.0%; Pred. No. 0.0015;
 Matches 22; Conservative 11; Mismatches 15; Indels 2; Gaps 1;
 QY 1 MFTLKSLLLFLPLGTINSLCEERDADDERDDLE--ERDVEVEKRF 48
 DB 1 MSFLKSLLLFLPLGLVSLVCKEERTEENENHEEGSEMRY 50
 RESULT 12
 A35514
 [D-Ala(2)] deltorphin precursor - two-colored leaf frog
 C:Species: Phyllomedusa bicolor (two-colored leaf frog)
 C:Date: 31-Oct-1990 #sequence_revision 31-Oct-1990 #text_change 09-Jul-2004
 C:Accession: A35514
 R:Richter, K.; Egger, R.; Negri, L.; Corsi, R.; Severini, C.; Kreil, G.
 Proc. Natl. Acad. Sci. U.S.A. 87, 4836-4839, 1990
 A:Title: cDNAs encoding [D-Ala(2)]deltorphin precursors from skin of Phyllomedusa bicolor
 A:Reference number: A35514; MUID:90280471; PMID:2352951
 A:Accession: A35514
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-227 <RIC>
 A:Cross-references: UNIPROT:P21850; GB:M34560; NID:G213540; PID:AAA49451.1; PID:G213541
 C:Superfamily: dermatophin precursor; dermatophin precursor amino-terminal homology
 C:Keywords: skin
 F:1-48/Domain: dermatophin precursor amino-terminal homology <DER1>
 F:168-214/Domain: dermatophin precursor amino-terminal homology <DER2>
 Query Match 31.4%; Score 96; DB 2; Length 227;
 Best Local Similarity 46.9%; Pred. No. 0.0029;
 Matches 23; Conservative 11; Mismatches 13; Indels 2; Gaps 2;
 QY 1 MFTLKSLLLFLPLGTINSLC-EERDADDERDDLEERDVEVE-KRF 47
 DB 1 MSFLKSLLLFLPLGLVSHSVCKEERTEENENHEEGSEMRY 49
 RESULT 13
 A23723
 protein disulfide-isomerase (EC 5.3.4.1) Erp72 precursor - human
 N:Alternate names: endoplasmic reticulum protein Erp72
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1992 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 C:Accession: A23723; A36508
 R:Huang, S.H.; Tomich, J.W.; Wu, H.; Jong, A.; Holcenberg, J.
 J. Biol. Chem. 266, 5353, 1991
 A:Reference number: A23723; MUID:91161636; PMID:2002068
 A:Content: erratum
 A:Accession: A23723
 A:Molecule type: mRNA
 A:Residues: 1-645 <HUA>
 A:Cross-references: UNIPROT:P13667; GB:J05016; NID:G181507; PID:AAA58460.1; PID:G181508
 R:Huang, S.H.; Tomich, J.W.; Wu, H.; Jong, A.; Holcenberg, J.
 J. Biol. Chem. 264, 14762-14768, 1989

A;Title: Human deoxycytidine kinase. Sequence of cDNA clones and analysis of expression
 A;Reference number: A36508; MUID:89359272; PMID:2549034
 A;Accession: A36508
 A;Molecule type: DNA
 A;Residues: 1-609; 'TKRTQLNRVETEWSI' <HU2>
 A;Cross-references: GB:J05016
 A;Note: this sequence has been corrected reference A23723
 C;Comment: This sequence has no homology to deoxycytidine kinase (EC 2.7.1.74) and the P
 C;Genetics:
 A;Gene: GDB:BRP70; BRP72
 A;Superfamily: GDB:9957774
 C;Keywords: protein disulfide-isomerase; thioredoxin homology
 F;1-22/Domain: duplication; endoplasmic reticulum; intramolecular oxidoreductase; isomerase
 F;23-645/Product: endoplasmic reticulum protein ERp72 #status predicted <MAT>
 F;70-154/Domain: thioredoxin homology <TX1>
 F;185-269/Domain: thioredoxin homology <TX2>
 F;533-620/Domain: thioredoxin homology <TX3>
 F;642-645/Region: endoplasmic reticulum retention signal
 F;91-94,206-209,555-558/Disulfide bonds: redox-active #status predicted

Query Match 23.0%; Score 70.5; DB 1; Length 645;
 Best Local Similarity 28.2%; Pred. No. 5;
 Matches 20; Conservative 10; Mismatches 16; Indels 25; Gaps 2;
 QY 5 KKSLLLLFLGTLNLSLCE-----EERDAERDRDLERDVEVEKRPF 48
 Db 4 RKAFLLLLLQVLLAVAGSGPDEDSNRNNAIEDEEEEDDEDEEDLEVEKE-- 61
 QY 49 PVIGRIINGIL 59
 Db 62 -----NGVL 65

RESULT 14

F71896
 hypothetical protein jhp0718 - Helicobacter pylori (strain J99)
 C;Species: Helicobacter pylori
 A;Variety: strain J99
 C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
 R;Alm, R.A.; Ling, L.S.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
 Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
 Nature 397, 176-180, 1999
 A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
 A;Reference number: A71800; MUID:99120557; PMID:9923682
 A;Accession: F71896
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-429 <ARN>
 A;Cross-references: UNIPROT:Q9ZL62; GB:AE001503; GB:AE001439; MUID:g4155275; PIDN:AAD0630
 A;Experimental source: strain J99
 C;Genetics:
 A;Gene: jhp0718

Query Match 22.9%; Score 70; DB 2; Length 429;
 Best Local Similarity 41.3%; Pred. No. 3.8;
 Matches 19; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 10 LLFFLGLTNLSCEERDAERDRDLERDVEVEKRPFPVIGRI 55
 Db 130 LLAYLNTRNDNFIQVFDSESPKLEETYEKEKEKFPFIALL 175

RESULT 15

G69850
 hypothetical protein yjha - Bacillus subtilis
 C;Species: Bacillus subtilis
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C;Accession: G69850
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallert
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanlon,
 A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot,
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
 A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A;Reference number: A69580; MUID:98044033; PMID:9384377
 A;Accession: G69850
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-213 <KUN>
 A;Cross-references: UNIPROT:O34725; GB:Z99110; GB:AL009156; MUID:g2633472; PIDN:CAB13075.5
 A;Experimental source: strain 168
 C;Genetics:
 A;Gene: yjha
 C;Superfamily: Bacillus subtilis hypothetical protein yjha

Query Match 22.7%; Score 69.5; DB 2; Length 213;
 Best Local Similarity 43.2%; Pred. No. 2.2;
 Matches 19; Conservative 8; Mismatches 14; Indels 3; Gaps 2;
 QY 4 LKKSLLLLFLGTLNLSL--CEEERDAERDRDLERDVEVEK 45
 Db 1 MKKVVLLFLVLTIGLALSACSSSDASEKEKPEKKSQELRK 43

Search completed: March 30, 2005, 17:30:44

Job time : 45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 30, 2005, 17:30:01 ; Search time 140 Seconds
(without alignments)
144.265 Million cell updates/sec

Title: US-10-719-623A-16

Perfect score: 306

Sequence: 1 MFTLKSLLLFLGTINLS.....EVEKRFPPVIGRLNGILGK 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	306	100.0	61	15	US-10-719-623-16
2	103	33.7	78	15	Sequence 16, Appl
3	95	31.0	24	15	Sequence 2, Appl
4	70.5	23.0	1039	15	US-10-421-635-8
5	70	22.9	429	15	US-10-369-493-16475
6	70	22.9	430	15	US-10-335-977-6289
7	67.5	22.1	1189	15	US-10-335-977-6290
8	66	21.6	13	15	US-10-282-122A-45818
9	66	21.6	193	15	US-10-719-623-17
10	65.5	21.4	1192	9	US-10-424-599-245431
11	65.5	21.4	1192	15	US-09-815-242-10903
12	64	20.9	1684	16	US-10-282-122A-57178
13	63	20.6	59	14	US-10-408-765A-811
					Sequence 32735, A

14	62.5	20.4	705	9	US-09-925-302-531	Sequence 531, App
15	62.5	20.4	705	10	US-09-925-302-531	Sequence 531, App
16	62.5	20.4	763	15	US-10-428-487-9	Sequence 9, Appl
17	62	20.3	403	15	US-10-425-114-39578	Sequence 39578, A
18	62	20.3	549	9	US-09-764-864-1131	Sequence 1131, App
19	62	20.3	576	15	US-10-425-114-65214	Sequence 65214, A
20	62	20.3	586	15	US-10-425-114-70516	Sequence 70516, A
21	62	20.3	708	16	US-10-437-963-167468	Sequence 167468, A
22	61.5	20.1	286	15	US-10-424-599-282549	Sequence 282549, A
23	61	19.9	207	15	US-10-425-114-41590	Sequence 41590, A
24	60	19.6	64	9	US-09-864-761-45501	Sequence 45501, A
25	60	19.6	367	15	US-10-425-114-48334	Sequence 48334, A
26	60	19.6	605	9	US-09-860-298-2	Sequence 2, Appl
27	60	19.6	605	10	US-09-832-129-37	Sequence 37, Appl
28	60	19.6	605	11	US-09-833-245-2237	Sequence 2237, App
29	60	19.6	605	14	US-10-028-072-160	Sequence 160, App
30	60	19.6	605	14	US-10-140-808-160	Sequence 160, App
31	60	19.6	605	14	US-10-121-049-160	Sequence 160, App
32	60	19.6	605	14	US-10-123-904-160	Sequence 160, App
33	60	19.6	605	14	US-10-140-470-160	Sequence 160, App
34	60	19.6	605	14	US-10-175-746-160	Sequence 160, App
35	60	19.6	605	14	US-10-176-918-160	Sequence 160, App
36	60	19.6	605	14	US-10-137-921-160	Sequence 160, App
37	60	19.6	605	14	US-10-137-865-160	Sequence 160, App
38	60	19.6	605	14	US-10-140-474-160	Sequence 160, App
39	60	19.6	605	14	US-10-142-431-160	Sequence 160, App
40	60	19.6	605	14	US-10-143-114-160	Sequence 160, App
41	60	19.6	605	14	US-10-142-419-160	Sequence 160, App
42	60	19.6	605	14	US-10-123-262-160	Sequence 160, App
43	60	19.6	605	14	US-10-142-423-160	Sequence 160, App
44	60	19.6	605	14	US-10-121-050-160	Sequence 160, App
45	60	19.6	605	14	US-10-141-755-160	Sequence 160, App

ALIGNMENTS

RESULT 1

US-10-719-623-16
; Sequence 16, Application US/10719623
; Publication No. US20040073977A1
; GENERAL INFORMATION:
; APPLICANT: Miera and Kay
; TITLE OF INVENTION: Transgenic Plants that are Resistant to a Broad Spectrum
; FILE OF INVENTION: of Pathogens
; FILE REFERENCE: 673243
; CURRENT APPLICATION NUMBER: US/10/719,623
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/125,072
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: PCT/CA00/00288
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 09/936,885
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Rana temporaria
US-10-719-623-16

Query Match 100.0%; Score 306; DB 15; Length 61;
Best Local Similarity 100.0%; Pred. No. 5.3e-29;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MFTLKSLLLFLGTINLSCEERDADDEERDDLEERDVEVEKRFPPVIGRLNGILG 60
Db	1	MFTLKSLLLFLGTINLSCEERDADDEERDDLEERDVEVEKRFPPVIGRLNGILG 60
Qy	61	K 61
Db	61	K 61

```
RESULT 2
US-10-719-623-2
; Sequence 2, Application US/10719623
; Publication No. US20040073977A1
; GENERAL INFORMATION:
; APPLICANT: Miera and Kay
; TITLE OF INVENTION: Transgenic Plants that are Resistant to a Broad Spectrum
; TITLE OF INVENTION: of Pathogens
; FILE REFERENCE: 673243
; CURRENT APPLICATION NUMBER: US/10/719,623
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/125,072
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: PCT/CA00/00288
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 09/936,885
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Phyllomedusa bicolor
US-10-719-623-2
Query Match      33.7%; Score 103; DB 15; Length 78;
Best Local Similarity 56.8%; Pred. No. 0.00011;
Matches 21; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

QY 1 MFTLKKSLLLPLGTLNLSLCEER--DADERDD 35
Db 1 MDILKKSLFLVLPLGLVLSICEKRENEDEKQDD 37

RESULT 3
US-10-421-635-8
; Sequence 8, Application US/10421635
; Publication No. US20040064847A1
; GENERAL INFORMATION:
; APPLICANT: Miera, Santosh et al.
; TITLE OF INVENTION: Transgenic Plants Exhibiting Resistance to a Spectrum
; FILE REFERENCE: 55682
; CURRENT APPLICATION NUMBER: US/10/421,635
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: US/09/616,110
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/165,249
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Rana temporaria
US-10-421-635-8
Query Match      31.0%; Score 95; DB 15; Length 24;
Best Local Similarity 75.0%; Pred. No. 0.00025;
Matches 18; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 23 EEERDAEERDDLEERDVEVEKR 46
Db 1 EEERNAEEERDDPERDQVEKR 24

RESULT 4
US-10-369-493-16475
; Sequence 16475, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16475
; LENGTH: 1039
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(1039)
; OTHER INFORMATION: unsure at all xaa locations
US-10-369-493-16475
Query Match      23.0%; Score 70.5; DB 15; Length 1039;
Best Local Similarity 41.2%; Pred. No. 16;
Matches 21; Conservative 6; Mismatches 7; Indels 17; Gaps 3;

QY 14 LGTNLSLCEER-ERDADE-----ERRDLE-----ERDVEVEKRF 47
Db 837 LGTNLGAIDVEYVAERHTFLLEQRDDLEAKATLHQLITMDEMKCRF 887

RESULT 5
US-10-335-977-6289
; Sequence 6289, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 6289:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 429 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
```


HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Helicobacter pylori
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...429
SEQUENCE DESCRIPTION: SEQ ID NO: 6289:
US-10-335-977-6289

Query Match 22.9%; Score 70; DB 15; Length 429;
Best Local Similarity 41.3%; Pred. No. 6.6;
Matches 19; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 10 LFFFLGTINLSCEERDAERDDLEERDVEVEKRFPPFVIGRIL 55
Db 130 LLAYLNRRNDFNIQVFDSEESPEKLETYKEIEKEKFFPIALL 175

RESULT 6
US-10-335-977-6290
; Sequence 6290, Application US/10335977
; Publication No. US20040052799A1
; GENERAL INFORMATION:
; APPLICANT: DOUGLAS SMITH et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO HELICOBACTER PYLORI FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 10031
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows NT 4.0
; SOFTWARE: UNIX
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/335,977
; FILING DATE: 30-Dec-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/993,002
; FILING DATE: 17-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: GTN-018
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 6290:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...430
; SEQUENCE DESCRIPTION: SEQ ID NO: 6290:
US-10-335-977-6290

Query Match 22.9%; Score 70; DB 15; Length 430;
Best Local Similarity 41.3%; Pred. No. 6.6;
Matches 19; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 10 LFFFLGTINLSCEERDAERDDLEERDVEVEKRFPPFVIGRIL 55

Db 131 LLAYLNRRNDFNIQVFDSEESPEKLETYKEIEKEKFFPIALL 176

RESULT 7
US-10-282-122A-45818
; Sequence 45818, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Cart, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45818
; TYPE: PRT
; LENGTH: 1189
; ORGANISM: Bacillus anthracis
US-10-282-122A-45818

Query Match 22.1%; Score 67.5; DB 15; Length 1189;
Best Local Similarity 39.2%; Pred. No. 42;
Matches 20; Conservative 7; Mismatches 7; Indels 17; Gaps 3;

QY 14 LCTINLSCEE-ERDAE-----ERRDDLE-----ERDVEVEKRF 47
Db 984 LCTVNLGAIDYERVAERHTFLLEQKDDLEAKTTLHQLITEMDEEMKKRF 1034

RESULT 8
US-10-719-623-17
; Sequence 17, Application US/10719623
; Publication No. US20040073977A1
; GENERAL INFORMATION:
; APPLICANT: Misra and Kay
; TITLE OF INVENTION: Transgenic Plants that are Resistant to a Broad Spectrum
; TITLE OF INVENTION: of Pathogens
; FILE REFERENCE: 673243
; CURRENT APPLICATION NUMBER: US/10/719,623

; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/125,072
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: PCT/CA00/00288
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 09/936,885
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Rana temporaria
US-10-719-623-17

Query Match 21.6%; Score 66; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 FFPVIGRIINGIL 59
DB 1 FFPVIGRIINGIL 13

RESULT 9
US-10-424-599-245431
; Sequence 245431, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 245431
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_63656C.1.pap
US-10-424-599-245431

Query Match 21.6%; Score 66; DB 15; Length 193;
Best Local Similarity 35.4%; Pred. No. 7.8;
Matches 17; Conservative 7; Mismatches 24; Indels 0; Gaps 0;

QY 13 FLGTINLSCEERDADERRDRLERDVEVEKRPFPVIGRIINGILG 60
DB 49 YASAIVSSSEVKGITQRIQHDLEGRRLALEKKFVPTVKARLKIGCG 96

RESULT 10
US-09-815-242-10903
; Sequence 10903, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242

; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10903
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10903

Query Match 21.4%; Score 65.5; DB 9; Length 1192;
Best Local Similarity 34.5%; Pred. No. 74;
Matches 20; Conservative 6; Mismatches 15; Indels 17; Gaps 2;

QY 14 LGTINLSCEERDADE-----ERRDDL-----EERDVEVEKRPFPVIGRI 54
DB 984 LGPVNLSAIEQFEQVDERHQFLVSQRDLDLNAKEQLFETMDMDQEVKRPKEVFEAL 1041

RESULT 11
US-10-282-122A-57178
; Sequence 57178, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034a
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57178
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-10-282-122A-57178

Query Match      21.4%; Score 65.5; DB 15; Length 1192;
Best Local Similarity 34.5%; Pred. No. 74;
Matches 20; Conservative 6; Mismatches 15; Indels 17; Gaps 2;

QY 14 LGPNLSLCEERDADSE-----ERDDL-----EERDVVEKRPFPVIGRI 54
Db 984 LGPNLSLAIEQFQVDERHQFLVSQRDLDLNAKEQLFETWDEMDQVKGKFEVFBAI 1041

RESULT 12
US-10-408-765A-811
; Sequence 811, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Pabhy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 811
; LENGTH: 1684
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-811

Query Match      20.9%; Score 64; DB 16; Length 1684;
Best Local Similarity 54.2%; Pred. No. 1.7e+02;
Matches 13; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 23 EERDADEERRDDLEERDVVEKRP 46
Db 113 EEEEEDEERKOSDERQKKKKR 136

RESULT 13
US-10-029-386-32735
; Sequence 32735, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32735
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004493.1
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; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.7
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.5
US-10-029-386-32735

Query Match      20.6%; Score 63; DB 14; Length 59;
Best Local Similarity 40.0%; Pred. No. 4.5;
Matches 12; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

QY 23 EERDADEERRDDLEERDVVEKRPFPVIG 52
Db 25 EEEEEEEDEDEEELELELELRLPRLAG 54

RESULT 14
US-09-925-302-531
; Sequence 531, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 531
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-531

Query Match      20.4%; Score 62.5; DB 9; Length 705;
Best Local Similarity 51.9%; Pred. No. 91;
Matches 14; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 23 EERDADEERRDDLEERDVVEKRPFP 49
Db 226 EEEEEEEED-EEEDYDVYKSEFP 251

RESULT 15
US-09-925-302-531
; Sequence 531, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 531
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-531

Query Match      20.4%; Score 62.5; DB 10; Length 705;
Best Local Similarity 51.9%; Pred. No. 91;
Matches 14; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 23 EERDADEERRDDLEERDVVEKRPFP 49
Db 226 EEEEEEEED-EEEDYDVYKSEFP 251
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Search completed: March 30, 2005, 17:42:51
Job time : 141 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2005, 17:21:25 ; Search time 42 Seconds
(without alignments)
108.419 Million cell updates/sec

Title: US-10-719-623A-16

Perfect score: 306

Sequence: 1 MFTLKSLLLFFLGTINLS.....EVEKFFPVIGRLNGILGK 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/prodata/1/1aa/6A-COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B-COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCITUS-COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfilees1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	306	100.0	61	3	US-09-319-730-19
2	306	100.0	61	4	US-09-936-885A-16
3	245	80.1	61	3	US-09-319-730-15
4	219.5	71.7	58	3	US-09-319-730-17
5	103	33.7	78	4	US-09-936-885A-2
6	70.5	23.0	645	4	US-09-538-092-920
7	66	21.6	13	3	US-09-319-730-7
8	66	21.6	13	4	US-09-936-885A-17
9	65.5	21.4	1208	4	US-09-134-000C-5756
10	62.5	20.4	166	4	US-09-513-999C-5648
11	62.5	20.4	706	1	US-08-339-152A-29
12	62.5	20.4	706	2	US-08-007-999B-4
13	62.5	20.4	706	2	US-08-689-276A-4
14	62.5	20.4	763	1	US-08-155-331-13
15	62.5	20.4	763	1	US-08-424-022-13
16	62.5	20.4	763	2	US-08-424-017B-13
17	62.5	20.4	763	4	US-09-538-092-1272
18	62.5	20.4	763	5	PCT-US93-11696-13
19	62	20.3	932	4	US-09-248-796A-19128
20	61	19.9	95	3	US-09-134-001C-5627
21	60.5	19.8	103	3	US-09-134-001C-4292
22	60	19.6	605	3	US-09-394-645-2
23	60	19.6	605	3	US-09-243-560B-2
24	60	19.6	3457	2	US-08-416-603-4
25	59.5	19.4	180	4	US-09-569-804-35
26	59.5	19.4	361	4	US-09-107-532A-4446
27	59.5	19.4	462	4	US-09-543-681A-5241

28 59.5 19.4 576 4 US-09-519-232-4 Sequence 4, Appli
29 58.5 19.1 608 4 US-09-270-767-3937 Sequence 3237, A
30 58.5 19.1 608 4 US-09-270-767-48154 Sequence 48154, A
31 58 19.0 388 4 US-09-248-796A-18781 Sequence 18781, A
32 58 19.0 590 4 US-09-248-796A-18990 Sequence 18990, A
33 58 19.0 1898 1 US-08-056-200-94 Sequence 94, Appl
34 58 19.0 1898 2 US-08-800-644-94 Sequence 94, Appl
35 58 19.0 1898 4 US-09-538-092-1280 Sequence 1280, Ap
36 57.5 18.8 822 4 US-09-328-352-5754 Sequence 5754, Ap
37 57.5 18.8 1382 4 US-09-171-991-9 Sequence 9, Appli
38 57.5 18.8 1388 4 US-09-949-016-10817 Sequence 10817, A
39 57 18.6 61 4 US-09-248-796A-25881 Sequence 25881, A
40 57 18.6 87 4 US-09-248-796A-22150 Sequence 22150, A
41 57 18.6 183 4 US-09-107-532A-5644 Sequence 5644, Ap
42 57 18.6 315 4 US-09-585-645A-42 Sequence 42, Appl
43 57 18.6 437 4 US-09-538-092-876 Sequence 876, App
44 57 18.6 568 4 US-09-949-016-10896 Sequence 10896, A
45 57 18.6 587 4 US-09-538-092-1130 Sequence 1130, Ap

ALIGNMENTS

RESULT 1
US-09-319-730-19
; Sequence 19, Application US/09319730
; Patent No. 6310176
; GENERAL INFORMATION:
; APPLICANT: BARRA, Donatella
; APPLICANT: SIMMACO, Maurizio
; TITLE OF INVENTION: ANTIMICROBIALY ACTIVE POLYPEPTIDES
; FILE REFERENCE: 003300-574
; CURRENT APPLICATION NUMBER: US/09/319,730
; CURRENT FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: PCT/SE97/02075
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: SE 9604593-5
; PRIOR FILING DATE: 1996-12-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 19
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Rana Temporaria
; US-09-319-730-19

Query Match 100.0%; Score 306; DB 3; Length 61;
Best Local Similarity 100.0%; Pred. No. 7.8e-31;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MFTLKSLLLFFLGTINLSLCEERDADEERDDLEERDVEKRFPPVIGRLNGILG 60
Db 1 MFTLKSLLLFFLGTINLSLCEERDADEERDDLEERDVEKRFPPVIGRLNGILG 60
Qy 61 K 61
Db 61 K 61

RESULT 2
US-09-936-885A-16
; Sequence 16, Application US/09936885A
; Patent No. 6835868
; GENERAL INFORMATION:
; APPLICANT: Misra and Kay
; TITLE OF INVENTION: Transgenic Plants that are Resistant to a Broad Spectrum
; TITLE OF INVENTION: of Pathogens
; FILE REFERENCE: 60993
; CURRENT APPLICATION NUMBER: US/09/936,885A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/125,072
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: PCT/CA00/00288

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; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Rana temporaria
US-09-936-885A-16

Query Match
Best Local Similarity 100.0%; Score 306; DB 4; Length 61;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFTLKSLLLPFLGTINLSLCEERDADERRDDLEERDVEVEKRFPPVIGRIILNGILG 60
Db 1 MFTLKSLLLPFLGTINLSLCEERDADERRDDLEERDVEVEKRFPPVIGRIILNGILG 60

QY 61 K 61
Db 61 K 61

RESULT 3
US-09-319-730-15
; Sequence 15, Application US/09319730
; Patent No. 6310176
; GENERAL INFORMATION:
; APPLICANT: BARRA, Donatella
; APPLICANT: SIMMACO, Maurizio
; TITLE OF INVENTION: ANTIMICROBIALY ACTIVE POLYPEPTIDES
; FILE REFERENCE: 003300-574
; CURRENT APPLICATION NUMBER: US/09/319,730
; CURRENT FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: PCT/S897/02075
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: SE 9604593-5
; PRIOR FILING DATE: 1996-12-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Rana Temporaria
US-09-319-730-15

Query Match
Best Local Similarity 80.1%; Score 245; DB 3; Length 61;
Matches 46; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 MFTLKSLLLPFLGTINLSLCEERDADERRDDLEERDVEVEKRFPPVIGRIILNGILG 60
Db 1 MFTLKSLLLPFLGTINLSLCEERDADERRDDLEERDVEVEKRFPPVIGRIILNGILG 60

QY 61 K 61
Db 61 K 61

RESULT 4
US-09-319-730-17
; Sequence 17, Application US/09319730
; Patent No. 6310176
; GENERAL INFORMATION:
; APPLICANT: BARRA, Donatella
; APPLICANT: SIMMACO, Maurizio
; TITLE OF INVENTION: ANTIMICROBIALY ACTIVE POLYPEPTIDES
; FILE REFERENCE: 003300-574
; CURRENT APPLICATION NUMBER: US/09/319,730
; CURRENT FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: PCT/S897/02075
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: SE 9604593-5
; PRIOR FILING DATE: 1996-12-13

; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Rana Temporaria
US-09-319-730-17

Query Match
Best Local Similarity 71.7%; Score 219.5; DB 3; Length 58;
Matches 45; Conservative 7; Mismatches 6; Indels 3; Gaps 1;

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Db 1 MFTLKSLLLPFLGTINLSLCEERDADERRDDLEERDVEVEKRFPPVIGRIILNGILG 57

QY 61 K 61
Db 58 K 58

RESULT 5
US-09-936-885A-2
; Sequence 2, Application US/09936885A
; Patent No. 6835868
; GENERAL INFORMATION:
; APPLICANT: Misra and Kay
; TITLE OF INVENTION: Transgenic Plants that are Resistant to a Broad Spectrum
; FILE OF INVENTION: of Pathogens
; FILE REFERENCE: 60993
; CURRENT APPLICATION NUMBER: US/09/936,885A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/125,072
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: PCT/CA00/00288
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Phyllomedusa bicolor
US-09-936-885A-2

Query Match
Best Local Similarity 33.7%; Score 103; DB 4; Length 78;
Matches 21; Conservative 8; Mismatches 6; Indels 2; Gaps 1;

QY 1 MFTLKSLLLPFLGTINLSLCEER--DADERRDD 35
Db 1 MDILKSLFLVFLGLVSLICEEKRENEDEEKQDD 37

RESULT 6
US-09-538-092-920
; Sequence 920, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 920
; LENGTH: 645
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(6)
; OTHER INFORMATION: Polypeptide Accession Number P13667
US-09-538-092-920

Query Match      23.0%; Score 70.5; DB 4; Length 645;
Best Local Similarity 28.2%; Pred. No. 1.5;
Matches 20; Conservative 10; Mismatches 16; Indels 25; Gaps 2;

QY 5 KKSLLLLFFLGLTINLSLCE-----BERDADEERRDDDLERDVEVEKRF 48
Db 4 RKAFLLLLLLGLVQLAVAGAGPDESDSSNRNAREDEBEREDDEEDDDLEVKEE-- 61

QY 49 FVIGRIILNGIL 59
Db 62 -----NGVL 65

RESULT 7
US-09-319-730-7
; Sequence 7, Application US/09319730
; Patent No. 6310176
; GENERAL INFORMATION:
; APPLICANT: BARRA, Donatella
; APPLICANT: SIMMACO, Maurizio
; TITLE OF INVENTION: ANTIMICROBIALY ACTIVE POLYPEPTIDES
; FILE REFERENCE: 003300-574
; CURRENT APPLICATION NUMBER: US/09/319,730
; CURRENT FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: PCT/SE97/02075
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: SE 9604593-5
; PRIOR FILING DATE: 1996-12-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Rana Temporaria
US-09-319-730-7

Query Match      21.6%; Score 66; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 FFPVIGRIILNGIL 59
Db 1 FFPVIGRIILNGIL 13

RESULT 8
US-09-936-885A-17
; Sequence 17, Application US/09936885A
; Patent No. 6835868
; GENERAL INFORMATION:
; APPLICANT: Misra and Kay
; TITLE OF INVENTION: Transgenic Plants that are Resistant to a Broad Spectrum
; FILE REFERENCE: 60993
; CURRENT APPLICATION NUMBER: US/09/936,885A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/125,072
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: PCT/CA00/00288
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Rana temporaria

US-09-936-885A-17

Query Match      21.6%; Score 66; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 FFPVIGRIILNGIL 59
Db 1 FFPVIGRIILNGIL 13

RESULT 9
US-09-134-000C-5756
; Sequence 5756, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5756
; LENGTH: 1208
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5756

Query Match      21.4%; Score 65.5; DB 4; Length 1208;
Best Local Similarity 34.5%; Pred. No. 13;
Matches 20; Conservative 6; Mismatches 15; Indels 17; Gaps 2;

QY 14 LGTINLSLCEERDADE-----ERRDDU-----ERDVEVEKRFPPVIGRI 54
Db 1000 LGFVNLSAIEQEQVDERHQFLVSRDDLLNAKEQLFETMDMDQVKEKRFKEVFEAI 1057

RESULT 10
US-09-513-999C-5648
; Sequence 5648, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5648
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 92
; OTHER INFORMATION: Xaa=Asp or Glu
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 94
; OTHER INFORMATION: Xaa=Asp or Glu or Gly
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 126
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; OTHER INFORMATION: Xaa=His or Arg
US-09-513-999C-5648

Query Match          20.4%; Score 62.5; DB 4; Length 166;
Best Local Similarity 51.9%; Pred. No. 3.3;
Matches 14; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 23 EERDADEERDDLEERDVVEKRFPP 49
Db 38 EEEDEEEEEEED-EEEDYDVYKSEFP 63

RESULT 11
US-08-339-152A-29
; Sequence 25, Application US/08339152A
; Patent No. 5643726
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovacs, Dora M.
; TITLE OF INVENTION: Methods For Modulating Transcription
; TITLE OF INVENTION: From The Amyloid -Protein Precursor (APP) Promoter
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Ave., NW, Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,152A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Steffe, Eric K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 0609.4120000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; TELEX:
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 706 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-339-152A-29

Query Match          20.4%; Score 62.5; DB 1; Length 706;
Best Local Similarity 51.9%; Pred. No. 17;
Matches 14; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 23 EERDADEERDDLEERDVVEKRFPP 49
Db 217 EEEDEEEEEEED-EEEDYDVYKSEFP 242

RESULT 12
US-08-007-999B-4
; Sequence 4, Application US/08007999B
; Patent No. 5851787
; GENERAL INFORMATION:
; APPLICANT: Wasco, Wilma
; APPLICANT: Bupp, Keith
; APPLICANT: Magendantz, Margaret
; APPLICANT: Tanzi, Rudolph
; APPLICANT: Solomon, Frank
; TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,276A
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; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/007,999B
; FILING DATE: 21-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,642
; FILING DATE: 20-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,022
; FILING DATE: 17-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: 0609.3520002/JAG/GKT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2571
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 706 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-007-999B-4

Query Match          20.4%; Score 62.5; DB 2; Length 706;
Best Local Similarity 51.9%; Pred. No. 17;
Matches 14; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 23 EERDADEERDDLEERDVVEKRFPP 49
Db 217 EEEDEEEEEEED-EEEDYDVYKSEFP 242

RESULT 13
US-08-689-276A-4
; Sequence 4, Application US/08689276A
; Patent No. 5891991
; GENERAL INFORMATION:
; APPLICANT: Wasco, Wilma
; APPLICANT: Bupp, Keith
; APPLICANT: Magendantz, Margaret
; APPLICANT: Tanzi, Rudolph
; APPLICANT: Solomon, Frank
; TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Ave., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/689,276A
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; FILING DATE: 06-AUG-1996
; PRIOR APPLICATION DATA: US 08/007,999
; APPLICATION NUMBER: 21-JAN-1993
; FILING DATE: 21-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,642
; FILING DATE: 20-APR-1992
; PRIOR APPLICATION DATA: US 07/930,022
; APPLICATION NUMBER: 17-AUG-1992
; FILING DATE: 17-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: JORGE A. GOLDSTEIN
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0609.3520003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)371-2571
; TELEFAX: (202)371-2540
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 706 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-689-276A-4

Query Match 20.4%; Score 62.5; DB 2; Length 706;
Best Local Similarity 51.9%; Pred. No. 17;
Matches 14; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 23 EEERADAEERRDDLEERDVEVEKRFPP 49
Db 217 EEEDEEEEEEED-EEEDYDVYKSEFP 242

RESULT 14
US-08-155-331-13
; Sequence 13, Application US/08155331
; Patent No. 5441931
; GENERAL INFORMATION:
; APPLICANT: Foster, Donald C
; APPLICANT: Sprecher, Cindy
; APPLICANT: No. 5441931ris, Kjeld
; TITLE OF INVENTION: NOVEL HUMAN AMYLOID PROTEIN PRECURSOR
; TITLE OF INVENTION: HOMOLOG AND KUNITZ-TYPE INHIBITOR
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/155,331
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,692
; FILING DATE: 02-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31-684
; REFERENCE/DOCKET NUMBER: 92-21C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-547-8080 ext 322
; TELEFAX: 206-548-2329
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 763 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-155-331-13

Query Match 20.4%; Score 62.5; DB 1; Length 763;
Best Local Similarity 51.9%; Pred. No. 18;
Matches 14; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 23 EEERADAEERRDDLEERDVEVEKRFPP 49
Db 216 EEEDEEEEEEED-EEEDYDVYKSEFP 241

RESULT 15
US-08-424-022-13
; Sequence 13, Application US/08424022
; Patent No. 5677146
; GENERAL INFORMATION:
; APPLICANT: Foster, Donald C
; APPLICANT: Sprecher, Cindy
; APPLICANT: No. 5677146ris, Kjeld
; TITLE OF INVENTION: NOVEL HUMAN AMYLOID PROTEIN PRECURSOR
; TITLE OF INVENTION: HOMOLOG AND KUNITZ-TYPE INHIBITOR
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,022
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,692
; FILING DATE: 02-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31-684
; REFERENCE/DOCKET NUMBER: 92-21C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-547-8080 ext 322
; TELEFAX: 206-548-2329
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 763 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-022-13

Query Match 20.4%; Score 62.5; DB 1; Length 763;
Best Local Similarity 51.9%; Pred. No. 18;
Matches 14; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

QY 23 EEERADAEERRDDLEERDVEVEKRFPP 49
Db 216 EEEDEEEEEEED-EEEDYDVYKSEFP 241

Search completed: March 30, 2005, 17:31:32
Job time : 43 secs

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OM protein - protein search, using sw model

Run on: March 30, 2005, 17:11:55 ; Search time 171 Seconds

(without alignments)
137.967 Million cell updates/sec

Title: US-10-719-623A-16

Perfect score: 306

Sequence: 1 MFTLKSLLLFLFLTNLS.....EVEKFFPVPVIGRLNGILGK 61

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	306	100.0	61	AAW51843	Aaw51843 Rana temp
2	306	100.0	61	AAW51843	Aab18737 A tempor
3	245	80.1	61	AAW51841	Aaw51841 Rana temp
4	219.5	71.7	58	AAW51842	Aaw51842 Rana temp
5	103	33.7	78	AAW518724	Aab18724 A dermase
6	95	31.0	24	AAW62384	Aag62384 Pro-regio
7	92	30.1	62	ADR88893	Adr88893 Amino aci
8	70.5	23.0	645	AAW66531	Aag66531 Human int
9	70.5	23.0	645	ADOL19794	Adol19794 Human PRO
10	70.5	23.0	645	ABM80947	Abm80947 Tumour-as
11	70.5	23.0	645	ADP56088	Adp56088 Human PRO
12	70.5	23.0	646	AAU30243	Aau30243 Novel hum
13	70.5	23.0	918	AAU30491	Aau30491 Novel hum
14	70.5	23.0	1039	ADS27442	Ads27442 Bacterial
15	70	22.9	429	AAV10949	Aay10949 H. pylori
16	70	22.9	430	AAW20585	Aaw20585 H. pylori
17	69	22.5	1512	ADM57239	Adm57239 A thalian
18	68	22.2	605	AAV57950	Aav57950 Human tra
19	67.5	22.1	91	AAU30488	Aau30488 Novel hum
20	67.5	22.1	1189	ABU17894	Abu17894 Protein e
21	66	21.6	13	AAW18738	Aab18738 Amino aci
22	66	21.6	122	ABG03927	Abg03927 Novel hum
23	66	21.6	164	ABG02975	Abg02975 Novel hum
24	66	21.6	164	ABG05363	Abg05363 Novel hum
25	66	21.6	199	ABG06330	Abg06330 Novel hum

26	66	21.6	283	5	ABU52101	Abu52101 Helicobac
27	66	21.6	429	4	AAW46342	Aab46342 H. pylori
28	66	21.6	429	4	AAW46342	Aab46342 H. pylori
29	65.5	21.4	1192	4	AAU35310	Aau35310 Enterococ
30	65.5	21.4	1192	6	ABU29254	Abu29254 Protein e
31	65.5	21.4	1208	7	ADH87871	Adh87871 Enterococ
32	65	21.2	365	4	ABW63283	Abw63283 Drosophil
33	64	20.9	1598	3	AAW30466	Aag30466 Arabidops
34	64	20.9	1599	3	AAW30465	Aag30465 Arabidops
35	64	20.9	1637	3	AAW41602	Aag41602 Arabidops
36	64	20.9	1684	3	AAW30464	Aag30464 Arabidops
37	64	20.9	1684	7	ADJ69005	Adj69005 Human hea
38	63.5	20.8	211	3	AAW23517	Aag23517 Arabidops
39	63.5	20.8	219	3	AAW23516	Aag23516 Arabidops
40	63.5	20.8	309	3	AAW23515	Aag23515 Arabidops
41	63.5	20.8	2478	4	ABB64182	Abb64182 Drosophil
42	63	20.6	59	8	ABO59101	Abos9101 Human gen
43	63	20.6	106	4	ABB68525	Abb68525 Drosophil
44	63	20.6	368	3	AAW44390	Aag44390 Arabidops
45	63	20.6	465	3	AAW44389	Aag44389 Arabidops

ALIGNMENTS

RESULT 1
AAW51843
ID AAW51843 standard; protein; 61 AA.

XX AAW51843;

XX 26-OCT-1998 (first entry)

XX Rana temporaria temporin G peptide.

XX Temporin G; anti-microbial property; anti-fungal property.

XX Rana temporaria.

XX Key Location/Qualifiers

FT Peptide 1..22

FT Protein /note= "Signal peptide"

FT /note= "Mature temporin G peptide; this peptide is

FT claimed under claim 1 on page 20 in the specification"

FT Modified-site 59

FT /note= "C-terminal amide present in the mature peptide"

XX WO9825961-A1.

XX 18-JUN-1998.

XX 12-DEC-1997; 97WO-SE002075.

XX 13-DEC-1996; 96SE-00004593.

XX (SBLV-) SBL VACCIN AB.

XX Barra D, Simmaco M;

XX WPI, 1998-362423/31.

XX N-PSDB; AAV07449.

XX Peptides from the skin of the frog Rana temporaria - useful as anti-microbial or anti-fungal compositions.

XX Claim 1; Page 19, 20; 27pp; English.

XX The present sequence represents the Rana temporaria temporin G anti-microbial peptide encoded by the temporin G cDNA which was isolated from a R. temporaria skin cDNA library. The invention claims for other R. temporaria derived peptides which are claimed to be useful in medicaments for anti-microbial and anti-fungal use

```
XX SQ Sequence 61 AA;
Query Match 100.0%; Score 306; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 3.2e-30;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFTLKSLLLPFLGTINSLCEERDADEERDDLEERDVEVEKRPFPVIGRIILNGILG 60
DB 1 MFTLKSLLLPFLGTINSLCEERDADEERDDLEERDVEVEKRPFPVIGRIILNGILG 60

QY 61 K 61
DB 61 K 61

RESULT 2
AAB18737
ID AAB18737 standard; protein; 61 AA.
XX
AC AAB18737;
XX
DT 22-JAN-2001 (first entry)
XX
DE A temporin G precursor polypeptide.
XX
KW Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;
KW cationic peptide; pathogen resistance.
XX
OS Rana temporaria.
XX
PN WO200055337-A1.
XX
PD 21-SEP-2000.
XX
PF 16-MAR-2000; 2000WO-CA000288.
XX
PR 17-MAR-1999; 99US-0125072P.
XX
PA (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
XX
PI Misra S, Kay WD;
XX
DR WPI; 2000-647077/62.
DR N-PSDB; AAV75750.
XX
Transgenic plants resistant to broad spectrum of pathogens useful for
producing biologically active cationic peptides, comprises nucleic acid
molecule encoding temporin and/or dermaseptin peptides.
XX
PS Disclosure; Page 49-50; 58pp; English.
XX
The present sequence represents a temporin precursor polypeptide. The
specification also describes dermaseptin polypeptides. Temporin and
dermaseptin have antibacterial activity. Dermaseptin also inhibits fungal
growth. Cationic peptides derived from temporins and dermaseptins are
used to produce transgenic plants. The transgenic plants are useful for
producing biologically active cationic peptides such as temporins and
dermaseptins in large quantities. The peptide confers broad spectrum
pathogen resistance including enhanced resistance to both fungal and
bacterial pathogens in the transgenic plants. The transgenic plants may
be used in conventional agricultural applications such as food crops,
medical and other applications
XX SQ Sequence 61 AA;
Query Match 100.0%; Score 306; DB 3; Length 61;
Best Local Similarity 100.0%; Pred. No. 3.2e-30;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFTLKSLLLPFLGTINSLCEERDADEERDDLEERDVEVEKRPFPVIGRIILNGILG 60
DB 1 MFTLKSLLLPFLGTINSLCEERDADEERDDLEERDVEVEKRPFPVIGRIILNGILG 60

QY 61 K 61
DB 61 K 61

us-10-719-623a-16.rag
QY 61 K 61
DB 61 K 61

RESULT 3
AAW51841
ID AAW51841 standard; protein; 61 AA.
XX
AC AAW51841;
XX
DT 26-OCT-1998 (first entry)
XX
DE Rana temporaria temporin B peptide.
XX
KW Temporin B; anti-microbial property; anti-fungal property.
XX
OS Rana temporaria.
XX
FH Key Location/Qualifiers
FT Peptide 1..22 /note= "Signal peptide"
FT Protein 47..59 /note= "Mature temporin B peptide; this peptide is
claimed under claim 1 on page 20 in the specification"
FT Modified-site 59 /note= "C-terminal amide present in the mature peptide"
XX
PN WO9825961-A1.
XX
PD 18-JUN-1998.
XX
PF 12-DEC-1997; 97WO-SE002075.
XX
PR 13-DEC-1996; 96SE-00004593.
XX
PA (SBLV-) SBL VACCIN AB.
XX
PI Barra D, Simmaco M;
XX
DR WPI; 1998-362423/31.
DR N-PSDB; AAV07447.
XX
Peptides from the skin of the frog Rana temporaria - useful as anti-
microbial or anti-fungal compositions.
XX
PS Claim 1; Page 18, 20; 27pp; English.
XX
The present sequence represents the Rana temporaria temporin B anti-
microbial peptide encoded by the temporin B cDNA which was isolated from
a R. temporaria skin cDNA library. The invention claims for other R.
temporaria derived peptides which are claimed to be useful in medicaments
for anti-microbial and anti-fungal use
XX SQ Sequence 61 AA;
Query Match 80.1%; Score 245; DB 2; Length 61;
Best Local Similarity 75.4%; Pred. No. 1.1e-22;
Matches 46; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 MFTLKSLLLPFLGTINSLCEERDADEERDDLEERDVEVEKRPFPVIGRIILNGILG 60
DB 1 MFTLKSLLLPFLGTINSLCEERDADEERDDLEERDVEVEKRPFPVIGRIILNGILG 60

QY 61 K 61
DB 61 K 61

RESULT 4
AAW51842
ID AAW51842 standard; protein; 58 AA.
```

XX AAW51842;
 XX 26-OCT-1998 (first entry)
 XX Rana temporaria temporin H peptide.
 XX Temporin H; anti-microbial property; anti-fungal property.
 XX Rana temporaria.
 XX Key Location/Qualifiers
 FT Peptide 1..22
 FT Protein /note="Signal peptide"
 FT Modified-site 47..56
 FT /note="Mature temporin H peptide; this peptide is
 FT claimed under claim 1 on page 20 in the specification"
 FT /note="C-terminal amide present in the mature peptide"
 XX WO9825961-A1.
 XX 18-JUN-1998.
 XX 12-DEC-1997; 97WO-SE002075.
 XX 13-DEC-1996; 96SE-00004593.
 XX (SBLV-) SBL VACCIN AB.
 XX Barra D, Simmaco M;
 XX WPI; 1998-362423/31.
 XX N-PSDB; AAV07448.
 XX Peptides from the skin of the frog Rana temporaria - useful as anti-
 XX microbial or anti-fungal compositions.
 XX Claim 1; Page 18, 20; 27pp; English.
 XX The present sequence represents the Rana temporaria temporin H anti-
 XX microbial peptide encoded by the temporin H cDNA which was isolated from
 XX a R. temporaria skin cDNA library. The invention claims for other R.
 XX temporaria derived peptides which are claimed to be useful in medicaments
 XX for anti-microbial and anti-fungal use
 XX Sequence 58 AA;
 SQ
 Query Match 71.7%; Score 219.5; DB 2; Length 58;
 Best Local Similarity 73.8%; Pred. No. 1.6e-19;
 Matches 45; Conservative 7; Mismatches 6; Indels 3; Gaps 1;
 QY 1 MFTLKSLLLFLGLTINLSLCEERDDEERDDLEERDVEVEKFFVIGRIILNGILG 60
 DB 1 MFTLKSLLLFLGLTINLSLCEERNABEERDDEERDQVQVKRLSP---NLKSLLG 57
 QY 61 K 61
 DB 58 K 58
 RESULT 5
 AAB18724
 ID AAB18724 standard; protein; 78 AA.
 XX AAB18724;
 XX 22-JAN-2001 (first entry)
 XX A dermaseptin precursor polypeptide.
 XX Dermaeptin; antibacterial; fungal growth; temporin; transgenic plant;
 XX cationic peptide; pathogen resistance.

XX Phyllomedusa bicolor.
 XX WO200055337-A1.
 XX 21-SEP-2000.
 XX 16-MAR-2000; 2000WO-CA000288.
 XX 17-MAR-1999; 99US-0125072P.
 XX (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
 XX Misra S, Kay WD;
 XX WPI; 2000-647077/62.
 XX N-PSDB; AAA75749.
 XX Transgenic plants resistant to broad spectrum of pathogens useful for
 XX producing biologically active cationic peptides, comprises nucleic acid
 XX molecule encoding temporin and/or dermaseptin peptides.
 XX Disclosure; Page 47; 58pp; English.
 XX The present sequence represents a dermaseptin precursor polypeptide. The
 XX precursor is processed to produce two mature forms, dermaseptin b
 XX (AAB18725) and dermaseptin B (AAB18726). Dermaseptin has antibacterial
 XX activity, and inhibits fungal growth. Cationic peptides derived from
 XX temporins and dermaseptins are used to produce transgenic plants. The
 XX transgenic plants are useful for producing biologically active cationic
 XX peptides such as temporins and dermaseptins in large quantities. The
 XX peptide confers broad spectrum pathogen resistance including enhanced
 XX resistance to both fungal and bacterial pathogens in the transgenic
 XX plants. The transgenic plants may be used in conventional agricultural
 XX applications such as food crops, medical and other applications
 XX Sequence 78 AA;
 SQ
 Query Match 33.7%; Score 103; DB 3; Length 78;
 Best Local Similarity 56.8%; Pred. No. 6e-05;
 Matches 21; Conservative 8; Mismatches 6; Indels 2; Gaps 1;
 QY 1 MFTLKSLLLFLGLTINLSLCEER--DADERDD 35
 DB 1 MDILKSLFLVLFLGLVLSLICEERKRENEDEKQDD 37
 RESULT 6
 AAG62384
 ID AAG62384 standard; peptide; 24 AA.
 XX AAG62384;
 XX 30-AUG-2001 (first entry)
 XX Pro-region of temporin G peptide.
 XX Transgenic plant; cationic peptide; cecropin-mellitin; CEMA; resistance;
 XX antibacterial; antifungal; antimicrobial; food crop; blight; soft rot;
 XX frog; temporin G.
 XX Rana temporaria.
 XX WO200136647-A1.
 XX 25-MAY-2001.
 XX 14-JUL-2000; 2000WO-CA000826.
 XX 12-NOV-1999; 99US-0165249P.
 XX (UYVI-) UNIV VICTORIA INNOVATION & DEV CORP.
 XX

PI Misra S., Kay WD., Osavsky M;
 XX WPI; 2001-336007/35.
 XX Transgenic plants useful as food crops are resistant to late blight due
 XX to Phytophthora infestans and/or to soft rot due to Erwinia carotovara.
 XX Disclosure; Page 51; 55pp; English.
 XX The present invention relates to a transgenic plant, which expressed a
 CC cationic peptide of the cecropin-mellitin (CEMA) family or related
 CC peptide. CEMA is an antimicrobial peptide with confers resistance to
 CC fungal and bacterial pathogens. Included in the invention are CEMA-
 CC related fusion peptides in which an N-terminal extension peptide is fused
 CC to the CEMA peptide. A pro-region peptide may be used as a fusion
 CC peptide, which neutralises the cationic nature of the CEMA or CEMA-
 CC related peptide and provides enhanced stability in cellular environments,
 CC or decreases the toxicity of the CEMA or CEMA-related peptide to the host
 CC organism. Transgenic plants of the invention may be used in conventional
 CC agricultural applications, such as food crops. The plants may display
 CC resistance to late blight due to Phytophthora infestans and or to soft
 CC rot due to Erwinia carotovara. The present sequence represents a temporin
 CC G pro region peptide, which can be used to modify the CEMA peptides used
 CC in the invention
 XX Sequence 24 AA;
 SQ
 Query Match 31.0%; Score 95; DB 4; Length 24;
 Best Local Similarity 75.0%; Pred. No. 0.00016;
 Matches 18; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 23 EERDADERRDDLEDRDVEVKR 46
 DB 1 EEERNAEERDDEPDRDQVEKR 24
 RESULT 7
 ADR88893
 ID ADR88893 standard; protein; 62 AA.
 AC ADR88893;
 XX 18-NOV-2004 (first entry)
 DT Amino acid sequence of tryptophyllin-1 designated PdT-1.
 DE
 XX tryptophyllin-1; PdT-1; vasodilatory; frog; defensive skin secretion;
 KW vasodilation; ischaemic heart disease; ischaemic disease;
 KW vascular stenosis; occlusion; hypertension; blood-brain barrier;
 KW anti-cancer; angiogenesis; healing; transplant; graft;
 KW spinal cord injury; cardiovascular disease; arterial smooth muscle;
 KW central nervous system disorder; infection; inflammation; cancer; tumour;
 KW Hodgkin's disease; non-Hodgkin's lymphoma; multiple myeloma;
 KW haematopoietic malignancy; glaucoma; pulmonary hypertension; stroke;
 KW atherosclerosis; asthma; ophthalmologic disease; renal failure;
 KW menstrual disorder; obstetric condition; wound; gastroenteric disease;
 KW anaphylactic shock; endotoxic shock.
 XX Pachymedusa dactinolor.
 OS
 XX Key Location/Qualifiers
 FH Peptide 1..20
 FT /note= "signal peptide"
 FT Protein 21..62
 FT /note= "mature protein"
 XX WO2004074312-A2.
 PN
 XX 02-SEP-2004.
 PD
 XX 04-FEB-2004; 2004WO-IB000806.
 PF
 XX 05-FEB-2003; 2003GB-00002621.
 PR

PR 06-JUN-2003; 2003GB-00012990.
 XX (UVUL-) UNIV ULSTER.
 PA (SHAW/) SHAW C.
 PA (HRS/) HIRST D.
 PA (CHEN/) CHEN T.
 PA (OROU/) O'ROURKE M.
 XX Shaw C, Hirst D, Chen T, O'rouke M;
 PI WPI; 2004-642491/62.
 XX N-PSDB; ADR88892.
 DR Isolated tryptophyllin peptide obtained from biologically active analog
 XX of Pachymedusa dactinolor tryptophyllin-1, having vasodilatory activity,
 PT useful for treating conditions of vascular insufficiency e.g., ischemic
 PT heart disease.
 PS Disclosure; SEQ ID NO 18; 55pp; English.
 XX The present sequence represents a full length tryptophyllin-1, derived
 CC from Pachymedusa dactinolor and designated PdT-1. The specification
 CC describes tryptophyllin-1 peptides and PdT-1 analogues which have a
 CC vasodilatory activity. Tryptophyllin-1 peptides are isolated from frog
 CC defensive skin secretions. Tryptophyllin-1 peptides of the invention are
 CC useful for preparing a medicament for treating disorders where
 CC vasodilation is beneficial, such as ischaemic heart disease, ischaemic
 CC disease of other organs or organ systems, vascular stenoses, occlusion to
 CC peripheral vessels, or hypertension, and for increasing the transport of
 CC biologically active compounds across the blood-brain barrier, where the
 CC biologically active compound is an anti-cancer drug. They are useful for
 CC promoting angiogenesis, for treating conditions of vascular
 CC insufficiency, to promote healing at sites of transplantation and
 CC grafting, and for treating spinal cord injuries. They are also useful for
 CC treating cardiovascular disease, for increasing vasodilation, for
 CC treating hypertension, for dilating arterial smooth muscle. In
 CC combination with other therapeutic agents, peptides of the invention are
 CC useful for treating disorders in the brain including central nervous
 CC system disorder, bacterial, viral and fungal infections, inflammation and
 CC cancer, tumour, Hodgkin's disease, non-Hodgkin's lymphomas, multiple
 CC myeloma and haematopoietic malignancies. Tryptophyllin-1 peptides of the
 CC invention are also useful in treating glaucoma, pulmonary hypertension,
 CC stroke, atherosclerosis, asthma, ophthalmologic disease, renal failure,
 CC menstrual disorder, obstetric conditions, wound, gastroenteric disease,
 CC anaphylactic or endotoxic shock, etc.
 XX Sequence 62 AA;
 SQ
 Query Match 30.1%; Score 92; DB 8; Length 62;
 Best Local Similarity 44.4%; Pred. No. 0.0011;
 Matches 16; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
 QY 4 LKKSLLLLFFGLGTINLSCEERDADEERDDLEER 39
 DB 4 LKKSFLVLFLGFSISFCDEEKQDDDEGNEREEK 39
 RESULT 8
 AAG66531
 ID AAG66531 standard; protein; 645 AA.
 XX AAG66531;
 XX 22-OCT-2001 (first entry)
 DT Human interferon-alpha induced polypeptide, ERP-70.
 DE
 XX Human; interferon-alpha induced gene; type I interferon treatment;
 KW chronic viral hepatitis; relapsing remitting multiple sclerosis;
 KW neoplastic disease; ERP-70.
 XX Homo sapiens.
 OS

PN WO200159155-A2.
 XX 16-AUG-2001.
 XX 09-FEB-2001; 2001WO-GB000578.
 XX 11-FEB-2000; 2000GB-00003203.
 PR 11-FEB-2000; 2000GB-00003204.
 PR 11-FEB-2000; 2000GB-00003205.
 PR 11-FEB-2000; 2000GB-00003206.
 PR 11-FEB-2000; 2000GB-00003207.
 PR 11-FEB-2000; 2000GB-00003208.
 PR 11-FEB-2000; 2000GB-00003210.
 PR 11-FEB-2000; 2000GB-00003212.
 PR 11-FEB-2000; 2000GB-00003213.
 PR 11-FEB-2000; 2000GB-00003215.
 PR 11-FEB-2000; 2000GB-00003216.
 PR 11-FEB-2000; 2000GB-00003219.
 PR 11-FEB-2000; 2000GB-00003220.
 PR 11-FEB-2000; 2000GB-00003221.
 PR 11-FEB-2000; 2000GB-00003222.
 PR 17-FEB-2000; 2000GB-00003768.
 XX (PHAR-) PHARMA PACIFIC PTY LTD.
 PA Meritet J, Dron M, Tovey MG;
 XX WPI; 2001-483570/52.
 DR N-PSDB; AAH76458.
 XX Predicting responsiveness of a patient to treatment with a type I
 PT interferon comprising determining the level of induced proteins after
 PT treatment with a type I interferon.
 XX Claim 1; Page 58-60; 133pp; English.
 PS The invention relates to a method for predicting responsiveness of a
 CC patient to treatment with a type I interferon. The method comprises
 CC determining the level of one or more proteins with a 646, 164, 126, 598,
 CC 98, 177, 761, 361, 941, 657, 817, 429, 473, 399, 285 or 303 amino acid
 CC sequence fully defined in the specification after treatment with a type I
 CC interferon. The method allows a physician to determine whether a patient
 CC suffering from chronic viral hepatitis, neoplastic disease or relapsing
 CC remitting multiple sclerosis will respond favourably to Type I interferon
 CC treatment via oromucosal administration. The present sequence is one of
 CC the polypeptides listed above that may be used in the method
 XX Sequence 645 AA;
 Query Match 23.0%; Score 70.5; DB 4; Length 645;
 Best Local Similarity 28.2%; Pred. No. 6.7;
 Matches 20; Conservative 10; Mismatches 16; Indels 25; Gaps 2;
 OY 5 KKSLLLLFLGTLINLSLCE-----EERDADERRDDLEERDVEVEKRF 48
 Db 4 RKAFLLLLGLVQLLAVAGAGPDSNSRNAIEDDEEEEDDEEDDLEVKEE-- 61
 OY 49 PVIGRLNGIL 59
 Db 62 -----NGVL 65
 RESULT 9
 ID ADO19794
 XX ADO19794 standard; protein; 645 AA.
 AC ADO19794;
 XX 12-AUG-2004 (first entry)
 DT Human PRO polypeptide #359.
 DE Human; PRO; immune related disorder; systemic lupus erythematosus;
 XX
 KW

KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.
 XX Homo sapiens.
 OS WO2004043361-A2.
 PN 27-MAY-2004.
 PD 06-NOV-2003; 2003WO-US035269.
 PF 08-NOV-2002; 2002US-0425235P.
 PR (GETH) GENENTECH INC.
 PA Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 PI Wood WI, Wu TD;
 PI WPI; 2004-420067/39.
 DR N-PSDB; ADO19793.
 XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 PT treating an immune related disorder such as systemic lupus erythematosus,
 PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 PT spondyloarthropathy.
 XX Claim 7; SEQ ID NO 718; 1731pp; English.
 XX The invention relates to human PRO polypeptides and the polynucleotides
 CC encoding them. The polypeptides and polynucleotides are useful for
 CC treating and diagnosing immune related disorders in mammals. The immune
 CC related disorders include systemic lupus erythematosus, rheumatoid
 CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 CC mellitus, immune-mediated renal disease, demyelinating diseases of the
 CC central or peripheral nervous system, demyelinating polyneuropathy,
 CC Guillain-Barre syndrome and chronic inflammatory demyelinating
 CC polyneuropathy. This sequence represents a human PRO polypeptide of the
 CC invention.
 XX Sequence 645 AA;
 Query Match 23.0%; Score 70.5; DB 8; Length 645;
 Best Local Similarity 28.2%; Pred. No. 6.7;
 Matches 20; Conservative 10; Mismatches 16; Indels 25; Gaps 2;
 OY 5 KKSLLLLFLGTLINLSLCE-----EERDADERRDDLEERDVEVEKRF 48
 Db 4 RKAFLLLLGLVQLLAVAGAGPDSNSRNAIEDDEEEEDDEEDDLEVKEE-- 61
 OY 49 PVIGRLNGIL 59
 Db 62 -----NGVL 65
 RESULT 10
 ID ABM80947
 XX ABM80947 standard; protein; 645 AA.
 AC ABM80947;
 XX 18-NOV-2004 (first entry)
 DT Tumour-associated antigenic target (TAT) polypeptide PRO2733, SEQ:2443.
 DE Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 XX tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW

colorectal cancer; lung cancer; ovarian cancer; liver cancer;
central nervous system cancer; bladder cancer; pancreatic cancer;
cervical cancer; melanoma; leukaemia; hybridisation probe;
chromosome identification; chromosome mapping; gene mapping;
gene therapy; cytostatic.

Homo sapiens.

WO2004030615-A2

15-APR-2004.

29-SEP-2003: 2003WO-IIS028547.

02-OCT-2002: 2002US-0414971P.

(GETH) GENENTECH INC.

Wu TD, Zhang Z, Zhou Y:

WPI: 2004-347921/32.

N-PSDB; ACN38739.

New tumor-associated antigenic target polypeptides and nucleic acids, useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.

Claim 12: SEO ID NO 2443: 7273pp: English.

The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides may be overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention.

Sequence 645 AA:

23.0%: Score 70.5: DB 8: Length 645:

Local Similarity 28.2%; Pred. No. 6.7;

atches 20; Conservative 10; Mismatches 16; Indels 25; Gaps 2;

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5 KSLLLFFGLTINSLCE-----EERDADERRDDLEERDVEVEKRRFF 48
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4 RKAFLLLGLVQLLAVAGAECPDESSNRENAIEDEEEEEEDDEEDDLEVKEE-- 61

49 PVIGRILNGIL 59

62 -----NGVL 65

13

8809

ADP56088 standard; protein; 645 AA.

ADP56088:

18-NOV-2004 (first entry)

Human PRO protein sequence SEO ID NO:2064.

human; PRO: immune related disease, inflammatory immune response; immune response stimulation; antiallergic; antianaemic; antiarthritis; antiasthmatic; antidiabetic; antinflammatory; antipsoriatic; antirheumatic; antithyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatocytic; immunostimulant; immunosuppressive; muscular; neurotropic; neuroprotective; osteopathic; respiratory; vasotropic; virucide; gene therapy.

Homo sapiens

WO2004039956-A2.

13-MAY-2004.

28-OCT-2003: 2003WO-US034381.

29-OCT-2002: 2002US-0422472P.

(GETH) GENENTECH INC.

Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM; Wood WI. Wu TD:

WPT: 2004-376182/35.

N-PSDB: ADP56087.

New PRO polynucleotides and polypeptides, useful in useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in stimulating an immune response.

Claim 1: SEQ ID NO 264: 3009pp: English:

The present invention describes an isolated PRO nucleic acid (1). Also described: (1) a vector comprising (1); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptides; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the polypeptide of (4) fused to a heterologous amino acid sequence; (6) an antibody which specifically binds to a polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4), an agonist or antagonist of the polypeptide or an antibody that binds to the polypeptide in combination with a carrier; (8) an article of manufacture comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a mammal; (10) a method for determining the presence of a PRO polypeptide in a sample suspected of having the polypeptide; (11) a method of diagnosing an immune related disease or an inflammatory immune response in mammal; (12) a method of identifying a compound that inhibits or mimics the activity of or expression of a gene encoding a PRO polypeptide; and (13) a method of stimulating the immune response in a mammal. The PRO sequences have antiatheric, antianaemic, antiarthritic, antiasthmatic, antidiabetic, antiinflammatory, antipsoriatic, antirheumatic, antithyroid, CNS, dermatological, gastrointestinal, haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular, neurotrophic, neuroprotective, osteopathic, respiratory, vasotropic and virucide activities, and can be used in gene therapy. The nucleic acid (1) and the encoded polypeptides, compositions, kits and methods are useful in diagnosing and treating an immune related disease and in stimulating an immune response. The present sequence represents a human PRO protein from the present invention.

Sequence 645 AA:

ery Match 23.0%; Score 70.5; DB 8; Length 645;

st Local Similarity 28.2%; Pred. No. 6.7;

atches 20; Conservative 10; Mismatches 16; Indels 25; Gaps 2;

5 KKSLLLLFFLGTINLSLCE-----EERDADEERRDDLEERDVEVEKRFF, 48

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4 RKAFLLLLLLGLVQLLAVAGAEGPDSSNRNAIEDDEEEEDDDDEEDDLEVKEE-- 61
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QY 49 PVIGRILNGIL 59
Db 62 -----NGVL 65

RESULT 12
AAU30243
ID AAU30243 standard; protein; 646 AA.

XX AC AAU30243;
XX DT 18-DEC-2001 (first entry)
XX DE Novel human secreted protein #734.

XX KW Human; vaccination; gene therapy; nutritional supplement;
XX KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX OS Homo sapiens.

XX PN WO200179449-A2.

XX PD 25-OCT-2001.

XX PF 16-APR-2001; 2001WO-US008656.

XX PR 18-APR-2000; 2000US-00552929.

XX PR 26-JAN-2001; 2001US-00770160.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-611725/70.

XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic
XX PT vaccination, testing and therapy.

XX PS Claim 20; Page 266; 765pp; English.

XX CC The invention relates to novel human secreted polypeptides. The
XX CC polypeptides and antibodies to the polypeptides are useful for
XX CC determining the presence of or predisposition to a disease associated
XX CC with altered levels of polypeptide. The polypeptides are also useful for
XX CC identifying agents (agonists and antagonists) that bind to them. Cells
XX CC expressing the proteins are useful for identifying a therapeutic agent
XX CC for use in treatment of a pathology related to aberrant expression or
XX CC physiological interactions of the polypeptide. Vectors comprising the
XX CC nucleic acids encoding the polypeptides and cells genetically engineered
XX CC to express them are also useful for producing the proteins. The proteins
XX CC are useful in genetic vaccination, testing and therapy, and can be used
XX CC as nutritional supplements. They may be used to increase stem cell
XX CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
XX CC and/or nerve tissue growth or regeneration; immune suppression and/or
XX CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
XX CC AAU29510-AAU3304 represent the amino acid sequences of novel human
XX CC secreted proteins of the invention

XX SQ Sequence 646 AA;

Query Match 23.0%; Score 70.5; DB 4; Length 646;
Best Local Similarity 28.2%; Pred. No. 6.7;
Matches 20; Conservative 10; Mismatches 16; Indels 25; Gaps 2;

QY 5 KKSLLLLPLGTLINSLCE-----EERDADERRDDLEERDVEVEKRPF 48

Db 4 RKAFLLLGLLVQLAVAGAGPDESSNRNATEDDEEEEDDEEDDLVKEE-- 61

QY 49 PVIGRILNGIL 59

Db 62 -----NGVL 65

RESULT 13
AAU30491

XX ID AAU30491 standard; protein; 918 AA.

XX AC AAU30491;

XX DT 18-DEC-2001 (first entry)

XX DE Novel human secreted protein #982.

XX KW Human; vaccination; gene therapy; nutritional supplement;

XX KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;

XX KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX OS Homo sapiens.

XX PN WO200179449-A2.

XX PD 25-OCT-2001.

XX PF 16-APR-2001; 2001WO-US008656.

XX PR 18-APR-2000; 2000US-00552929.

XX PR 26-JAN-2001; 2001US-00770160.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Drmanac RT;

XX DR WPI; 2001-611725/70.

XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic
XX PT vaccination, testing and therapy.

XX PS Claim 20; Page 300; 765pp; English.

XX CC The invention relates to novel human secreted polypeptides. The
XX CC polypeptides and antibodies to the polypeptides are useful for
XX CC determining the presence of or predisposition to a disease associated
XX CC with altered levels of polypeptide. The polypeptides are also useful for
XX CC identifying agents (agonists and antagonists) that bind to them. Cells
XX CC expressing the proteins are useful for identifying a therapeutic agent
XX CC for use in treatment of a pathology related to aberrant expression or
XX CC physiological interactions of the polypeptide. Vectors comprising the
XX CC nucleic acids encoding the polypeptides and cells genetically engineered
XX CC to express them are also useful for producing the proteins. The proteins
XX CC are useful in genetic vaccination, testing and therapy, and can be used
XX CC as nutritional supplements. They may be used to increase stem cell
XX CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
XX CC and/or nerve tissue growth or regeneration; immune suppression and/or
XX CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
XX CC AAU29510-AAU3304 represent the amino acid sequences of novel human
XX CC secreted proteins of the invention

XX SQ Sequence 918 AA;

Query Match 23.0%; Score 70.5; DB 4; Length 918;
Best Local Similarity 28.2%; Pred. No. 9.9;
Matches 20; Conservative 10; Mismatches 16; Indels 25; Gaps 2;

QY 5 KKSLLLLPLGTLINSLCE-----EERDADERRDDLEERDVEVEKRPF 48

Db 4 RKAFLLLGLLVQLAVAGAGPDESSNRNATEDDEEEEDDEEDDLVKEE-- 61

QY 49 PVIGRILNGIL 59

Db 62 -----NGVL 65

RESULT 14
AUS27442

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 17:57:33 ; Search time 295 Seconds
(without alignments)

6750.067 Million cell updates/sec

Title: US-10-719-623A-15

Perfect score: 329

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	329	100.0	329	17	US-10-719-623-15
2	45	13.7	443	17	Sequence 15, Appl
3	42.4	12.9	665	13	Sequence 1, Appl1
4	42.4	12.9	665	17	Sequence 185531,
5	40.6	12.3	403	11	Sequence 185531,
6	40.2	12.2	4804	18	Sequence 4267, Ap
7	40	12.2	56153	17	Sequence 30217, A
8	39.4	12.0	894	13	Sequence 520, App
9	39.4	12.0	894	17	Sequence 3788, Ap
10	39.4	12.0	8781	17	Sequence 3788, Ap
11	38.8	11.8	1746	18	Sequence 1659, App
					Sequence 116, App

12	38.6	11.7	466	9	US-09-864-761-16328	Sequence 16328, A
13	38.6	11.7	2211	17	US-10-424-599-44115	Sequence 44115, A
14	38.6	11.7	4756	9	US-09-982-091A-3	Sequence 3, Appli
15	38.6	11.7	23934	9	US-09-764-860-777	Sequence 777, App
16	38.6	11.7	23934	9	US-09-764-877-2536	Sequence 2536, Ap
17	38.6	11.7	23934	9	US-09-764-877-2544	Sequence 2544, Ap
18	38.6	11.7	23934	10	US-09-764-891-7210	Sequence 7210, Ap
19	38.6	11.7	23934	14	US-10-074-095-777	Sequence 777, App
20	38.6	11.7	23934	17	US-10-212-872-777	Sequence 777, App
21	38.6	11.7	23934	17	US-10-242-515-2536	Sequence 2536, Ap
22	38.6	11.7	23934	17	US-10-242-515-2544	Sequence 2544, Ap
23	38.4	11.7	14950	15	US-10-311-455-1230	Sequence 1230, Ap
24	38	11.6	477	13	US-10-027-632-20397	Sequence 20397, A
25	38	11.6	477	17	US-10-027-632-20397	Sequence 20397, A
26	38	11.6	765	9	US-09-974-300-8246	Sequence 8246, Ap
27	38	11.6	220860	17	US-10-684-190-3	Sequence 3, Appli
28	37.4	11.4	815	18	US-10-739-930-545	Sequence 545, App
29	37.4	11.4	640681	9	US-09-790-988-1	Sequence 1, Appli
30	37	11.2	433	9	US-09-878-178-1348	Sequence 1348, Ap
31	37	11.2	433	13	US-10-046-935-1348	Sequence 1348, Ap
32	37	11.2	433	14	US-10-146-502-1348	Sequence 1348, Ap
33	37	11.2	17738	15	US-10-311-455-1511	Sequence 1511, Ap
34	36.8	11.2	370	17	US-10-424-599-44029	Sequence 44029, A
35	36.8	11.2	381	18	US-10-425-115-28644	Sequence 28644, A
36	36.8	11.2	1176	14	US-10-156-275-5	Sequence 5, Appli
37	36.8	11.2	5495	14	US-10-156-275-1	Sequence 1, Appli
38	36.8	11.2	5495	14	US-10-156-275-2	Sequence 2, Appli
39	36.8	11.2	10592	14	US-10-156-275-51	Sequence 51, Appl
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41	36.8	11.2	10592	14	US-10-156-275-52	Sequence 52, Appl
42	36.8	11.2	10592	14	US-10-156-275-52	Sequence 52, Appl
43	36.6	11.1	6215	15	US-10-311-455-1164	Sequence 1164, Ap
44	36.4	11.1	598	13	US-10-027-632-218332	Sequence 218332,
45	36.4	11.1	598	13	US-10-027-632-218333	Sequence 218333,

ALIGNMENTS

RESULT 1

US-10-719-623-15
; Sequence 15, Application US/10719623
; Publication No. US20040073977A1
; GENERAL INFORMATION:
; APPLICANT: Misra and Kay
; TITLE OF INVENTION: Transgenic Plants that are Resistant to a Broad Spectrum
; TITLE OF INVENTION: of Pathogens
; FILE REFERENCE: 673243
; CURRENT APPLICATION NUMBER: US/10719, 623
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/125,072
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: PCT/CA00/00288
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 09/936,885
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 329
; TYPE: DNA
; ORGANISM: Rana temporaria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (53)..(238)
US-10-719-623-15

Query Match 100.0%; Score 329; DB 17; Length 329;
Best Local Similarity 100.0%; Pred. No. 3.9e-78;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	181	GGAAGAGAGATTTTCTCCAGTGTATTGGAAGGATACTCAATGGTATTTTGGGAAAATAACC	240
Db	181	GGAAGAGAGATTTTCTCCAGTGTATTGGAAGGATACTCAATGGTATTTTGGGAAAATAACC	240
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RESULT 2
US-10-719-623-1
; Sequence 1, Application US/10719623
; Publication No. US20040073977A1
; GENERAL INFORMATION:
; APPLICANT: Mirra and Kay
; TITLE OF INVENTION: Transgenic Plants that are Resistant to a Broad Spectrum
; TITLE OF INVENTION: of Pathogens
; FILE NUMBER: 673243
; CURRENT APPLICATION NUMBER: US/10/719,623
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/125,072
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: PCT/CA00/00288
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 09/936,885
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Phyllomedusa bicolor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (58)..(294)
US-10-719-623-1

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RESULT 3
US-10-027-632-185531
; Sequence 185531, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129

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, CURRENT APPLICATION NUMBER: US/10/027,632
, CURRENT FILING DATE: 2002-04-30
, PRIOR APPLICATION NUMBER: US 60/218,005
, PRIOR FILING DATE: 2000-07-12
, PRIOR APPLICATION NUMBER: US 60/198,676
, PRIOR FILING DATE: 2000-04-20
, PRIOR APPLICATION NUMBER: US 60/193,483
, PRIOR FILING DATE: 2000-03-29
, PRIOR APPLICATION NUMBER: US 60/185,218
, PRIOR FILING DATE: 2000-02-24
, PRIOR APPLICATION NUMBER: US 60/167,363
, PRIOR FILING DATE: 1999-11-23
, PRIOR APPLICATION NUMBER: US 60/156,358
, PRIOR FILING DATE: 1999-09-28
, PRIOR APPLICATION NUMBER: US 60/146,002
, PRIOR FILING DATE: 1999-08-09
, NUMBER OF SEQ ID NOS: 325720
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 185531
, LENGTH: 665
, TYPE: DNA
, ORGANISM: Human
, FEATURES:
, NAME/KEY: misc_feature
, LOCATION: (1)...1665)
, OTHER INFORMATION: n = A,T,C or G
US-10-027-632-185531

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	Query Match	12.9%	Score 42.4	DB 13	Length 665
	Best Local Similarity	53.7%	Pred. No. 0.46		
	Matches 88	Conservative 0	Mismatches 76	Indels 0	Gaps 0
Qy	166	AAGGATGTTGAAGTGGAAAGCCATTTTTTCCAGTGATTCGGAAGGATACCTCAATGGTAT	225		
Db	7	AAGATAAATTTTAATTTAAAAATGCTTCTTCCTAGTCTCTTCGCATATCCATACTAAAT	66		
Qy	226	TTTGGGAAATAACCAAAAAAAGTTAAAACTTTGGAATGGAATGGAATCATCTAATG	285		
Db	67	TTTATGTAACAATCAAACTATACCTATTTTTCGAGGAATGAATACATATTTATATAATT	126		
Qy	286	TGGAATGTCATTTAGCTAAAATGCGACATCAAAATGCTTTTAAAAA	329		
Db	127	TGGAGCATATCTCTGTCATTTTACAGAAAAATATCTATATATA	170		

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RESULT 4
US-10-027-632-185531
; Sequence 185531, Application US/10027632
; Publication No. US20030204075A9
;
GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,350
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185531

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; LENGTH: 665
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(665)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-185531

Query Match      12.9%; Score 42.4; DB 17; Length 665;
Best Local Similarity 53.7%; Pred. No. 0.46;
Matches 88; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 166 AAGCGATGTTGAAGTGGAAAGCGATTTTCCAGTGTGGAGGAGTACTCATGTAT 225
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 226 TTTGGGAAATTAACCAAAAAAGTTAAACCTTTTGGAAATGGAATGGAATCATCTAATG 285
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 286 TGGATGCTATTAGCTAAATGACATCAATGCTTTATATAAAA 329
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 127 TGGAGGAATATCTTTGTGATTTTACAGAAAATTATCTATATA 170
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
US-09-864-408A-4267/c
; Sequence 4267, Application US/09864408A
; Publication No. US2004009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shimkets, Richard A.
; TITLE OF INVENTION: No. US2004009474A1el Human Polynucleotides and Polypeptides Encod
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR FILING DATE: 2001-05-24
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4267
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-864-408A-4267

Query Match      12.3%; Score 40.6; DB 11; Length 403;
Best Local Similarity 51.4%; Pred. No. 1.1;
Matches 94; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

Qy 144 AAGAAGAGATGATCTCGAAGAAGGGATGTTGAAGTGGAAAAGCGATTTTTCAGTGA 203
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 293 ATACAAATGATCAGTAGCATATCTAGTGGCTCATGTGAAAGCAACTTTTCTCAGCTT 234
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 204 TTGGAAGGATCACTCAATGATTTTGGGAAAATAACCAAAAAAGTTAAACTTTGAAA 263
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 233 TAGTAAATATTTTCTAGATTTTGAAGAAGATAAAGCATTAATAATTTAGTATGAAGA 174
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 264 TGGAAATGGAATCATCTAATGGAATGTCATTTAGCTAAATGCACATCAATGCTTAA 323
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 324 TAA 326
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 113 TCA 111
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
US-10-357-930-30217
; Sequence 30217, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30217
; LENGTH: 4804
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 4776, 4777, 4778, 4779, 4780, 4781, 4782, 4783, 4784, 4785,
; LOCATION: 4786, 4787, 4788, 4789, 4790, 4791, 4792, 4793, 4794, 4795,
; LOCATION: 4796, 4797, 4798, 4799, 4800, 4801, 4802, 4803, 4804
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-30217

Query Match      12.2%; Score 40.2; DB 18; Length 4804;
Best Local Similarity 54.4%; Pred. No. 4.4;
Matches 81; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 120 AGGAAGAGAGATGCCGATGAGAGAGAGAGAGATGATCTCGAAGAAGGATTTTGAAG 179
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2074 AGGTAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2133
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 180 TGGAAAAGCGATTTTTCAGTGTGGAGGATCTCAATGGTATTTTGGAAAAATAAC 239
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2134 AGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2193
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 240 CAAAAAAGTTAAACTTTTGGAAATGGAA 268
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2194 CAAAAGATGAAAAAGAAATGGATAAGAA 2222
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
US-10-221-714A-520/c
; Sequence 520, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: tumor suppressor genes and oncogenes
; FILE REFERENCE: 5013,1005
; CURRENT APPLICATION NUMBER: US/10/221,714A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847,0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058,8
; PRIOR FILING DATE: 2000-04-06
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; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30217
; LENGTH: 4804
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 4776, 4777, 4778, 4779, 4780, 4781, 4782, 4783, 4784, 4785,
; LOCATION: 4786, 4787, 4788, 4789, 4790, 4791, 4792, 4793, 4794, 4795,
; LOCATION: 4796, 4797, 4798, 4799, 4800, 4801, 4802, 4803, 4804
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-30217

Query Match      12.2%; Score 40.2; DB 18; Length 4804;
Best Local Similarity 54.4%; Pred. No. 4.4;
Matches 81; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 120 AGGAAGAGAGATGCCGATGAGAGAGAGAGAGATGATCTCGAAGAAGGATTTTGAAG 179
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2074 AGGTAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2133
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 180 TGGAAAAGCGATTTTTCAGTGTGGAGGATCTCAATGGTATTTTGGAAAAATAAC 239
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2134 AGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2193
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 240 CAAAAAAGTTAAACTTTTGGAAATGGAA 268
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2194 CAAAAGATGAAAAAGAAATGGATAAGAA 2222
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
US-10-221-714A-520/c
; Sequence 520, Application US/10221714A
; Publication No. US20040048254A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: tumor suppressor genes and oncogenes
; FILE REFERENCE: 5013,1005
; CURRENT APPLICATION NUMBER: US/10/221,714A
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: PCT/EP01/02955
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: DE 10013847,0
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: DE 10019058,8
; PRIOR FILING DATE: 2000-04-06
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199 AGTGATTGGAAGGATCACTCAATGGTATTGTTGGAAAAATAACCAAAAAAGTTTAAACCTTT 258
287 AATCAAAAAACATAGACTCCAGGATTTCTTAGGGAAACAAACAAAGATTTTAAGACTTT 228
259 GGAATGGAATTTGGAATCATCTAA 283
227 AAAAATTAAATTTTATGTCCTTGAA 203

RESULT 9
US-10-027-632-3788/c
; Sequence 3788, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3788
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-3788

Query Match 12.0%; Score 39.4; DB 17; Length 894;
Best Local Similarity 54.5%; Pred. No. 3.3;
Matches 79; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 139 TGAAGAAAGAGATGATCTCGAAGAAAGGATGTTGAAGTGAAGGATTTTTC 198
Db 347 TCAAGATTTTACTCAGAAACCAATATTTGGAGACTTTACCAAGAACTCTATAGTCTCA 288
Qy 199 AGTGATTGGAAGGATCACTCAATGGTATTGTTGGAAAAATAACCAAAAAAGTTTAAACCTTT 258
Db 287 AATCAAAAAACATAGACTCCAGGATTTCTTAGGGAAACAAACAAAGATTTTAAGACTTT 228
Qy 259 GGAATGGAATTTGGAATCATCTAA 283
Db 227 AAAAATTAAATTTTATGTCCTTGAA 203

RESULT 10
US-10-311-455-1659
; Sequence 1659, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: PIERBROCK, Christian
; APPLICANT: BEJLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detect
; TITLE OF INVENTION: Cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537

178 AGTGGAAAGCGATTTTTCAGTGATTGGAAGGATCACTCAATGGTATTGTTGGAAAAATA 237
9356 ACTCCATAACCAATTTCTCAAAATATCGTATTAACTTAAACAAATTTTAA 9297
238 ACCAAAAAAGTTTAAACTTTGGAATGGAATGGAATCATCTAATGTGGAATGTCATT 237
9296 ACATATTAAATTTTAAATTTTCAAAATTTAAATTTAAATTTCAACCTACATACACTTA 9237
298 TAGCTAAATGCATCAATGTCCTTATAAAA 329
9236 TACCTAAACCCCTAACAAATATATTTTAAATA 9205

RESULT 8
US-10-027-632-3788/c
; Sequence 3788, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3788
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-3788

Query Match 12.0%; Score 39.4; DB 13; Length 894;
Best Local Similarity 54.5%; Pred. No. 3.3;
Matches 79; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 139 TGAAGAAAGAGATGATCTCGAAGAAAGGATGTTGAAGTGAAGGATTTTTC 198
Db 347 TCAAGATTTTACTCAGAAACCAATATTTGGAGACTTTACCAAGAACTCTATAGTCTCA 288

RESULT 13
US-10-424

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 17:09:23 ; Search time 97 Seconds
(without alignment)
5549.846 Million cell updates/sec

Title: US-10-719-623A-15

Perfect score: 329
Sequence: 1 cccctccagctgtctacatt.....catcaaatgtctttataaaaa 329

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	329	100.0	329	3	US-09-319-730-18
2	329	100.0	329	4	US-09-936-885A-15
3	212.8	64.7	323	3	US-09-319-730-14
4	203.8	61.9	356	3	US-09-319-730-16
5	45	13.7	443	4	US-09-936-885A-1
6	40.6	12.3	7218	1	US-08-232-463-14
7	40.6	12.3	45983	4	US-09-949-016-17010
8	40.2	12.2	4756	4	US-09-949-016-4455
9	40	12.2	202111	4	US-09-949-016-13877
10	39.8	12.1	601	4	US-09-949-016-183626
11	39.2	11.9	1664976	4	US-08-916-421B-1
12	39.2	11.9	1664976	4	US-09-692-570-1
13	37.8	11.5	5852	1	US-07-867-106-2
14	37.4	11.4	640681	4	US-09-790-988-1
15	36.8	11.2	1176	1	US-08-602-010A-5
16	36.8	11.2	1176	1	US-08-680-726A-5
17	36.8	11.2	1176	3	US-09-092-409-5
18	36.8	11.2	5495	1	US-08-602-010A-1
19	36.8	11.2	5495	1	US-08-602-010A-2
20	36.8	11.2	5495	1	US-08-680-726A-1
21	36.8	11.2	5495	1	US-08-680-726A-2
22	36.8	11.2	5495	3	US-09-092-409-2
23	36.8	11.2	10592	1	US-08-680-726A-51
24	36.8	11.2	10592	1	US-08-680-726A-51
25	36.8	11.2	10592	1	US-08-680-726A-52
26	36.8	11.2	10592	1	US-08-680-726A-52
27	36.8	11.2	10592	1	US-08-680-726A-52

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28 36.8 11.2 10592 3 US-09-092-409-51 Sequence 51, Appl
c 29 36.8 11.2 10592 3 US-09-092-409-51 Sequence 51, Appl
30 36.8 11.2 10592 3 US-09-092-409-52 Sequence 52, Appl
c 31 36.8 11.2 10592 3 US-09-092-409-52 Sequence 52, Appl
32 36 10.9 1170 4 US-09-248-796A-9079 Sequence 9079, Ap
c 33 36 10.9 2781 3 US-08-749-522-4 Sequence 4, Appl
c 34 35.8 10.9 54531 4 US-09-949-016-16267 Sequence 16267, A
c 35 35.8 10.9 86877 4 US-09-949-016-15491 Sequence 15491, A
c 36 35.8 10.9 86877 4 US-09-949-016-15492 Sequence 15492, A
37 35.4 10.8 601 4 US-09-949-016-183766 Sequence 183766,
c 38 35.4 10.8 1338 4 US-09-543-681A-2029 Sequence 2029, Ap
c 39 35.4 10.8 89625 4 US-09-949-016-17012 Sequence 17012, A
c 40 35.4 10.8 152331 3 US-09-128-155-16 Sequence 16, Appl
41 35.4 10.8 176373 3 US-09-128-155-17 Sequence 17, Appl
42 35.4 10.8 1664976 4 US-08-916-421B-1 Sequence 1, Appl
c 43 35.4 10.8 1664976 4 US-09-692-570-1 Sequence 1, Appl
c 44 35.2 10.7 640681 4 US-09-790-988-1 Sequence 1, Appl
45 35 10.6 429 4 US-09-248-796A-7362 Sequence 7362, Ap

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ALIGNMENTS

RESULT 1

US-09-319-730-18

; Sequence 18, Application US/09319730

; Patent No. 6310176

; GENERAL INFORMATION:

; APPLICANT: BARRA, Donatella

; APPLICANT: SIMMACO, Maurizio

; TITLE OF INVENTION: ANTIMICROBIALY ACTIVE POLYPEPTIDES

; FILE REFERENCE: 003300-574

; CURRENT APPLICATION NUMBER: US/09/319,730

; CURRENT FILING DATE: 1999-08-24

; PRIOR APPLICATION NUMBER: PCT/SE97/02075

; PRIOR FILING DATE: 1997-12-12

; PRIOR APPLICATION NUMBER: SE 9604593-5

; PRIOR FILING DATE: 1996-12-13

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 18

; LENGTH: 329

; TYPE: DNA

; ORGANISM: Rana Temporaria

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (53)..(235)

US-09-319-730-18

Query Match 100.0%; Score 329; DB 3; Length 329;

Best Local Similarity 100.0%; Pred. No. 8.7e-80;

Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CCCTCCAGCTGTCTACATCTCTCATACCACTGAACCCGAGCCCAAGATGTTTCAAC 60
Db 1 CCCTCCAGCTGTCTACATCTCTCATACCACTGAACCCGAGCCCAAGATGTTTCAAC 60
Qy 61 CTGGAAGAAATCCCTCTTACTCTCTTCTTGGGACCACCACTTATCTCTCTGTGA 120
Db 61 CTGGAAGAAATCCCTCTTACTCTCTTCTTGGGACCACCACTTATCTCTCTGTGA 120
Qy 121 GGAAGAGAGAGATGCCGATGAAGAAAGAGATGATCTCGAAGAAAGGGATGTTGAAGT 180
Db 121 GGAAGAGAGAGATGCCGATGAAGAAAGAGATGATCTCGAAGAAAGGGATGTTGAAGT 180
Qy 181 GGAAGAGAGATGTTTCCAGTGATGGAAGATCACTCAATGGTATTTTGGAAATAAACC 240
Db 181 GGAAGAGAGATGTTTCCAGTGATGGAAGATCACTCAATGGTATTTTGGAAATAAACC 240
Qy 241 AAAAAAGTTTAAACTTTTGGAAATGGAATGGAATCATCTTAATGTGGAATGTCATTAG 300
Db 241 AAAAAAGTTTAAACTTTTGGAAATGGAATGGAATCATCTTAATGTGGAATGTCATTAG 300

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QY 301 CTAATGACATCAATCAATGCTTTATATAAAA 329
Db 301 CTAATGACATCAATCAATGCTTTATATAAAA 329

RESULT 2
US-09-936-885A-15
; Sequence 15, Application US/09936885A
; Patent No. 6835868
; GENERAL INFORMATION:
; APPLICANT: Misra and Kay
; TITLE OF INVENTION: Transgenic Plants that are Resistant to a Broad Spectrum
; FILE REFERENCE: 60993
; CURRENT APPLICATION NUMBER: US/09/936,885A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/125,072
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: PCT/CA00/00288
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 329
; TYPE: DNA
; ORGANISM: Rana temporaria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (53)..(238)
; US-09-936-885A-15

Query Match 100.0%; Score 329; DB 4; Length 329;
Best Local Similarity 100.0%; Pred. No. 8,7e-80;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTCCAGCTGTCTACATTCCTATACCACTGACCACTGACCCGAGCCCAAGAGATGTTCAAC 60
Db 1 CCCCTCCAGCTGTCTACATTCCTATACCACTGACCACTGACCCGAGCCCAAGAGATGTTCAAC 60

QY 61 CTGGAAGAAATCCCTCTTACTCTCTTCTCTTGGGACCACTCACTTATCTCTCTGTGA 120
Db 61 CTGGAAGAAATCCCTCTTACTCTCTTCTCTTGGGACCACTCACTTATCTCTCTGTGA 120

QY 121 GGAAGAGAGATGCCGATGAAGAAAGAGATGATCTGAAAGAGGGATGTTGAAGT 180
Db 121 GGAAGAGAGATGCCGATGAAGAAAGAGATGATCTGAAAGAGGGATGTTGAAGT 180

QY 181 GGAAGAGAGATGTTTCCAGTGATGGAAGGATCACTCAATGTTTGGGAAATTAACC 240
Db 181 GGAAGAGAGATGTTTCCAGTGATGGAAGGATCACTCAATGTTTGGGAAATTAACC 240

QY 241 AAAAAGTTAAACTTTTGGAAATGGAATGGAATCACTAAATGTTGAATGTCATTTAG 300
Db 241 AAAAAGTTAAACTTTTGGAAATGGAATGGAATCACTAAATGTTGAATGTCATTTAG 300

QY 301 CTAATGACATCAATGCTTTATATAAAA 329
Db 301 CTAATGACATCAATGCTTTATATAAAA 329

RESULT 3
US-09-319-730-14
; Sequence 14, Application US/09319730
; Patent No. 6310176
; GENERAL INFORMATION:
; APPLICANT: Barra, Donatella
; TITLE OF INVENTION: ANTIMICROBIALY ACTIVE POLYPEPTIDES
; FILE REFERENCE: 003300-574
; CURRENT APPLICATION NUMBER: US/09/319,730
; CURRENT FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: PCT/SE97/02075
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 356
; TYPE: DNA
; ORGANISM: Rana temporaria
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79)..(252)
; US-09-319-730-16

Query Match 61.9%; Score 203.8; DB 3; Length 356;
Best Local Similarity 81.7%; Pred. No. 7.9e-46;
Matches 267; Conservative 0; Mismatches 42; Indels 18; Gaps 2;

QY 3 CCTCCAGCTGTCTACATTTCTCATACCACTGAACCCGAGCCCAAGAGATGTTACCT 62
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29	CTTCCAGCGGTACATTCTGAGCAACCAACTGAACCTCCGAGCCCAAGATGTTCACT	88
63	TGAAGAAATCCCTCTTACTCTCTTTCTTCTGGGACCATCAACTTATCTCTCTGTGAGG	122
89	TGAAGAAATCCCTGTTACTCTCTTTTCTTGGGACCATCAACTTATCTCTCTGTGAGG	148
123	AAGAGAGAGATGCCGATGAAGAAAGAGAGATGATCTCGAAGAAAGGGATGTTGAAGTGG	182
149	AAGAGAAATGCGAAGAAAGAAAGAGATGAACCAAGATGAAAGGGATGTTCAAGTGG	208
183	AAAAGCGATTTTTCAGTGATGGAGGATCTCAATGGTATTTTGGGAAATTAACCA	242
209	AAAACGACTTTCACC-----AAACCTGCTCAAGAGCTGTTGGGAAATAACCA-	258
243	AAAAAGTTAAAACTTGGAAATGGAATGGAATCATCTAAATGCGAATGTCATTTAGCT	302
259	-----AAAATCTTAAGATGGAATGGAATCATCTGATGCGAATATCATTTAGCT	310
303	AAATGCACATCAATGTCTTATAAAA	329
311	AAATGCGCAACAGATGTCTTATTAAA	337

RESULT 5

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US-09-936-885A-1
; Sequence 1, Application US/09936885A
; Patent No. 6835868
; GENERAL INFORMATION:
; APPLICANT: Misra and Kay
; TITLE OF INVENTION: Transgenic plants that are Resistant to a Broad Spectrum
; TITLE OF INVENTION: of Pathogens
; FILE REFERENCE: 60993
; CURRENT APPLICATION NUMBER: US/09/936,885A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/125,072
; PRIOR FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: PCT/CA00/00288
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Phyllomedusa bicolor
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (58) .. (294)
US-09-936-885A-1

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Query Match	13.7%;	Score 45;	DB 4;	Length 443;
Best Local Similarity	65.3%;	Pred. No. 0.0096;		
Matches	66;	Conservative	0;	Mismatches 35; Indels 0; Gaps 0;

QY	44	AGCCCCAAGATGTTCACTTTGAAGAAATCCCTCTTACTCCTTTTCTCTTGGGACCATC	103
Db	49	AGAACAAACATGATATCCTTGAAGAAATCTCTTTCTGTATTATTCCTTGGATTGGTT	108
QY	104	AACTTATCTCTCTGTGAGGAAGAGAGAGATGCCGATGAAGA	144
Db	109	TCCTTTTCCATCTCTGTGAAGGAAGAAAGAGAAATGAAGA	149

RESULT 6

RE5001.8
 US-08-232-463-14/c
 ; Sequence 14, Application US/08232463
 ; Patent No. 5670367
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: DORNER, F.
 ; APPLICANT: SCHEIFLINGER, F.
 ; APPLICANT: FALKNER, F. G.
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
 ; NUMBER OF SEQUENCES: 52

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s
; US-08-232-463-14

Query Match          12.3%; Score 40.6; DB 1; I
Best Local Similarity 2.3%; Pred. No. 0.39;
Matches             4; Conservative 117; Mismatches 56;

QY      119 GAGGAAGAGAGATGCGCATGACGAAGAAGAGATGATCTC
DB       : :::::::::::::: ::::::::::::::::::::
DB       1237 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
QY      179 GTGGAAAGCGATTTTTTCCAGTGATTGGAAGGATACTCA
DB       : ::::: ::::: ::::: ::::: ::::: :::::
DB      1177 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR
QY      239 CCAAAAAAGTTAAACTTGTGGAATGGAATTGGAATCATCA
DB       : ::::: ::::: ::::: ::::: ::::: :::::
DB      1117 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR

RESULT 7
US-09-949-016-17010/c
; Sequence 17010, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08

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us-10-719-623a-15.rn1

```

; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17010
; LENGTH: 45983
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(45983)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17010

Query Match      12.3%; Score 40.6; DB 4; Length 45983;
Best Local Similarity 51.4%; Pred. No. 0.72;
Matches 94; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 144 AAAGAAGAGATGATCTCGAAGAAAGGATGTTGAAGTGGAAGGCGATTTTTCAGTGA 203
Db 34909 ATACAAATGATCATGATAGCAATATCTAGTGGCTCATGTGAAGCAACTTTTCTCAGCTT 34850

QY 204 TTGGAAGGATACCTCAATGTTATTTTGGGAAATAACCAAAAAGTTTAAACCTTTGGA 263
Db 34849 TAGTAAAAATATTCTAGATTTTGGGAAGATAGCAATTAATAATATGATGATGAAGA 34790

QY 264 TGGAAATGGAAATCATCTAATGTGGAATGTCATTAGCTAAATGCACATCAAAATGCTTTA 323
Db 34789 CAAACAGCTACATGCTATAGCAATATGTCATATTTCTCAATGGACATAGATGCTTCA 34730

QY 324 TAA 326
Db 34729 TCA 34727

RESULT 8
US-09-949-016-4455
; Sequence 4455, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4455
; LENGTH: 4756
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4455

Query Match      12.2%; Score 40.2; DB 4; Length 4756;
Best Local Similarity 54.4%; Pred. No. 0.43;
Matches 81; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 120 AGGAAGAGAGATGCCGATGAAGAAAGAGATGATCTCGAAGAGGAGTGTGAAG 179
Db 2030 AGGTAGAGAAGAAAGAAAGAGGAGAACTAGAGGAAGAGGAGGAAGAAAGAGGAGG 2089

QY 180 TCGAAAGCGATTTTTCAGTGATGGAAGGATCTCAATGTTATTTTGGAAAAATAC 239
Db 2090 AGGAAGAAGAAATCAGGAGCTGCAGATTCCTCTTAGTAGAAGAAATAGAAA 2149

QY 240 CAAAAAAGTTAAACCTTTGGAAATGGA 268
Db 2150 CAAAAGTGAAGAAAGAAATGGATAAGAA 2178

RESULT 9
US-09-949-016-13877/c
; Sequence 13877, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13877
; LENGTH: 20211
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(20211)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13877

Query Match      12.2%; Score 40; DB 4; Length 20211;
Best Local Similarity 53.9%; Pred. No. 1.7;
Matches 82; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 119 GAGGAAGAGAGATGCCGATGAAGAAAGAGATGATCTCGAAGAAAGGATGTTGAA 178
Db 154940 GAGGAAGATGAATTTGGAGACGTAGACAGAGAAAGCAACATCTGGGCTTTGGGA 154881

QY 179 GTCGAAAAGCGATTTTTCAGTGATGTTGGAAGATCTCAATGTTATTTTGGAAAAATAA 238
Db 154880 GCTGAAGAGGAGTTTATTTCTTAAACATAGTAGAAGCCATCAGAGGGTTTAAAGCAAGAA 154821

QY 239 CCAAAAAAGTTAAACTTTTGGAAATGGAATT 270
Db 154820 CATAAAATAATTTGTACATTATTAAGSCATTT 154789

RESULT 10
US-09-949-016-183626
; Sequence 183626, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183626
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-183626
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```

Query Match          12.1%; Score 39.8; DB 4; Length 601;
Best Local Similarity 51.4%; Pred. No. 0.27; Indels 0; Gaps 0;
Matches 92; Conservative 0; Mismatches 87;

QY 148 AAGAGATCTCGAAGAAAGGATGTTGAAGTGGAAAAGCGAATTTTCCAGTCAATGG 207
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 AAATGATCAGTAGCAATATCTAGTGGCTCATGTGAAGCAACTTTTTCTCAGCTTTAGT 60

QY 208 AAGGATCTCAATGCTATTTTGGGAAATACCAAAAAGTTAAAACTTTGGAATGGA 267
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AAAAATATTTCTAGATTTTGAAGAAGATAAAGCAATTAATAATTAGTATGAAGACAAA 120

QY 268 ATTGGAATCATCTAATGTGAATGCTATTAGCTAAATGCACATCAAAATGCTTTATAA 326
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 CAGCTACATGAGCTATAGTAATGCGCATATTTCTCAATGGACATAGTAATGCTTCATCA 179

RESULT 11
US-08-916-421B-1/c
; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; TITLE OF INVENTION: jannaschii
; PATENT NO. 6503729
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; CURRENT FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28222)..(28222)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (28257)..(28258)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84773)..(84773)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (84808)..(84808)
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; NAME/KEY: misc feature
; LOCATION: (84812)..(84812)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98120)..(98120)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (98159)..(98159)
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; NAME/KEY: misc feature
; LOCATION: (98239)..(98239)
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; NAME/KEY: misc feature
; LOCATION: (98266)..(98266)
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; LOCATION: (98343)..(98343)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (103998)..(103998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (148948)..(148948)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (163385)..(163385)
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; NAME/KEY: misc feature
; LOCATION: (191989)..(191989)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (191995)..(191995)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (231980)..(231980)
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; LOCATION: (234187)..(234187)
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; NAME/KEY: misc feature
; LOCATION: (234220)..(234220)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (234814)..(234814)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309398)..(309398)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (309418)..(309418)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (312837)..(312837)
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; NAME/KEY: misc feature
; LOCATION: (312993)..(312993)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (319226)..(319226)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (559167)..(559167)
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; NAME/KEY: misc feature
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; NAME/KEY: misc feature
; LOCATION: (600992)..(600992)
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; NAME/KEY: misc feature
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (657081)..(657081)
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; NAME/KEY: misc feature
; LOCATION: (657203)..(657203)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (674435)..(674435)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (682442)..(682442)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (713652)..(713652)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (741684)..(741684)
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; NAME/KEY: misc feature
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (779676)..(779676)
; OTHER INFORMATION: n equals a, t, c, or g

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Fri Apr 1 08:00:35 2005

us-10-719-623a-15.rn1

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; NAME/KEY: misc feature
; LOCATION: (855539)..(855539)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (871619)..(871619)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1084830)..(1084830)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1096846)..(1096846)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1119881)..(1119881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1130881)..(1130881)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1310988)..(1310988)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1313224)..(1313224)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1349473)..(1349473)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1349491)..(1349491)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1470091)..(1470091)
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; NAME/KEY: misc feature
; LOCATION: (1569020)..(1569020)
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; NAME/KEY: misc feature
; LOCATION: (1602912)..(1602912)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1603734)..(1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1637998)..(1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc feature
; LOCATION: (1664854)..(1664854)
; OTHER INFORMATION: n equals a, t, c, or g
; US-08-916-421B-1
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Query Match 11.9%; Score 39.2; DB 4; Length 1664976;
Best Local Similarity 50.5%; Pred. No. 5.8;
Matches 95; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 141 AGAAGAGAGATGATCTCGAAGAAAGGATGTTGAAGTGAAAGCGATTTTTCAG 200
DB 1641889 AAGACCTTAAGATTTCTTTGAAATAATGATTAAGACATTGTAAGATACTTTTGATG 1641830

QY 201 TGATTTGGAAGGATCTCAATGGTATTTTCGGAATAATAACCAAAAAAGTTAAACTTTGG 260
DB 1641829 AATTTTAAAGATAATTTAGGAATAATAAGACATAATATCTGAAAAAGTTGAAATAGTCA 1641770

QY 261 AATGGAATTTGGAATCTATCTATGTGGATGTCATTTAGCTAAATGCACATCAATGTC 320
DB 1641769 AAAAAAGTTAAAAATAATGAAATAATAAGAAATTTTGAATTTATTTACCTTAAAGAAA 1641710

QY 321 TTATATAA 328
DB 1641709 TTAGAGAA 1641702
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RESULT 12
US-09-692-570-1/c

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; Sequence 1, Application US/09692570
; Patent No. 6797466
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
; Patent No. 6797466
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275C1
; CURRENT APPLICATION NUMBER: US/09/692,570
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 08/916,421
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1664976
; TYPE: DNA
; ORGANISM: Methanococcus jannaschii
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Query Match 11.9%; Score 39.2; DB 4; Length 1664976;

Best Local Similarity 50.5%; Pred. No. 5.8;

Matches 95; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

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Qy 201 TGATTGGAAGGATCACTCAATGGTATTTTGGAAAAATACCAAAAAAGTTTAAAACTTGG 260
Db 1641829 AATTTTAAAGTAATTTGAGGAATATAAGACATATATCTGAAAAAGTTGAAATAGTCA 1641770
Qy 261 AAATGGAATTGGAAATCATCTAATGTGGAATGTCATTTAGCTAAATGCACATCAAAATGTC 320
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Qy 321 TTATATAA 328

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Db 1641709 TTAGAGAA 1641702

RESULT 13

US-07-867-106-2

; Sequence 2, Application US/07867106

; Patent No. 5389526

; GENERAL INFORMATION:

; APPLICANT: Slade, Martin B

; APPLICANT: Chang, Andy C M

; APPLICANT: Williams, Keith L

; TITLE OF INVENTION: Improved Plasmid Vectors for Cellular

; TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris

; STREET: One Liberty Place 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: USA

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/867,106

; FILING DATE: 19920625

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: AU PJ 7187

; APPLICATION NUMBER: PCT/AU90/00530

; FILING DATE: 02-NOV-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Feeney, Joanne Longo

; REGISTRATION NUMBER: 35,134

; REFERENCE/DOCKET NUMBER: RICE-0002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-568-3100

; TELEFAX: 215-568-3439

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5852 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; ANTI-SENSE: NO

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 2378..5038

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 2378..5038

US-07-867-106-2

Query Match 11.5%; Score 37.8; DB 1; Length 5852;

Best Local Similarity 52.2%; Pred. No. 2.1;

Matches 84; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

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Db 4955 GAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGAT 5014

QY 182 GAAAGCGATTTTCCATGATTTGAAGGATCTCAATGGTATTTTGGGAAATAACCA 241

Db 5015 GAAGATGAAGACGAGATGGTATTTGAATTCATCTTTAAATAATTAATAATAATA 5074

QY 242 AAAAAGTTAAACCTTGGAAATGGAAATTTGGAATCATCTA 282

Db 5075 AAAAAAAGATTTTCAATTTAATAATATACATATATA 5115

RESULT 14

US-09-790-988-1

; Sequence 1, Application US/09790988

; Patent No. 6632935

; GENERAL INFORMATION:

; APPLICANT: SHIGENOBU, SHUJI

; APPLICANT: WATANABE, HIDEKI

; APPLICANT: HATTORI, MASAHIRA

; APPLICANT: SAKAKI, YOSHIYUKI

; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS

; FILE REFERENCE: 081356/0159

; CURRENT APPLICATION NUMBER: US/09/790,988

; CURRENT FILING DATE: 2001-02-23

; PRIOR APPLICATION NUMBER: JP2000-107160

; PRIOR FILING DATE: 2000-04-07

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 640681

; TYPE: DNA

; ORGANISM: Buchnera sp.

US-09-790-988-1

Query Match 11.4%; Score 37.4; DB 4; Length 640681;

Best Local Similarity 51.5%; Pred. No. 13;

Matches 86; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

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Db 279356 GAAAAAATCAAGATCCAAAAATAAATCATAAAAAATATGACAGTGATAATTTAATAAA 279415

QY 185 AAGCGATTTTTCAGTGTGGAAGGATCTCAATGGTATTTTGGGAAATAACCAAA 244

Db 279416 AAAAAATTTAATTCATTTTAGAAATACAACTAAAGAACTGAAAGAAATAATAGAA 279475

QY 245 AAAGTTAAAACTTTGGAATGGAATTTGGAATCATCTAATGTGGAAT 291

Db 279476 AAAGAGAAATAGTTGAAAGAAATAGTAAATACATAATAGATT 279522

RESULT 15

US-08-602-010A-5/c

; Sequence 5, Application US/08602010A

; Patent No. 5753235

; GENERAL INFORMATION:

; APPLICANT: Haanes, Elizabeth J.

; APPLICANT: Frank, Rexann S.

; TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sheridan Ross & McIntosh

; STREET: 1700 Lincoln Street, Suite 3500

; CITY: Denver

; STATE: Colorado

; COUNTRY: U.S.A

; ZIP: 80203

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/602,010A

; FILING DATE: February 15, 1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Connell, Gary J.

; REGISTRATION NUMBER: 32,020

; REFERENCE/DOCKET NUMBER: 2618-46

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 303/863-9700

; TELEFAX: 303/863-0223

; INFORMATION FOR SEQ ID NO: 5:


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 1176 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1176
US-08-602-010A-5

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Best Local Similarity 58.0%; Pred. No. 2.2;
Matches 65; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Job time : 105 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 14:45:33 ; Search time 1389 Seconds
(without alignments)
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Title: US-10-719-623A-15

Perfect score: 329

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	329	100.0	329	6	ARI176040	ARI176040 Sequence
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4	329	100.0	329	6	BD063212	BD063212 Antimicro
5	217.8	66.2	347	5	S69903	S69903 Ranalexin-a
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12	195.8	59.5	363	5	REBRE1E	X77831 R.esculenta
13	165.4	50.3	318	5	RRU22393	U22393 Rana rugosa
14	149.6	45.5	294	5	ARI427746	ARI427746 Rana pipi
15	125.4	38.1	362	5	RP1414584	AJ414584 Rana pipi
16	120	36.5	317	5	RP1427747	AJ427747 Rana pipi
17	119.8	36.4	310	5	AJ583866	AJ583866 Rana temp
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22	92	28.0	417	5	RP1427748	AJ427748 Rana pipi	
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DEFINITION	Y09395				
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VERSION	Y09395.1	GI:1771591			
KEYWORDS	temporin G.				
SOURCE	Rana temporaria (common frog)				
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REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana; Rana.				
AUTHORS	Simmaco, M., Mignogna, G., Canofeni, S., Miele, R., Mangoni, M.L. and Barra, D.				
TITLE	Temporins, antimicrobial peptides from the European red frog Rana temporaria				
JOURNAL	Eur. J. Biochem. 242 (3), 788-792 (1996)				
MEDLINE	97175050				
PUBMED	9022710				
REFERENCE	2 (bases 1 to 329)				
AUTHORS	Barra, D.				
TITLE	Direct Submission				
JOURNAL	Submitted (11-NOV-1996) D. Barra, Universita La Sapienza, Dipartimento Di Scienze Biochimiche, Piazzale Aldo Moro 5, 00185 Roma, ITALY				
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/notes="amidated C-terminus; post-translational
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/evidence=experimental

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Best Local Similarity 100.0%; Pred. No. 1.6e-65;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 CTTGAAGAAATCCCTCTTACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 120
QY 121 GGAAGAGAGAGATGCCGATCGAAGAAAGAGAGATGATCTCGAAGAAAGGATGTTGAAGT 180
DB 121 GGAAGAGAGAGATGCCGATCGAAGAAAGAGAGATGATCTCGAAGAAAGGATGTTGAAGT 180
QY 181 GGAAGAGAGATGTTTCCAGTGTGTTGGAAGGATCTCAATGGTATTTTGGGAAAATAAAC 240
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QY 241 AAAAAAGTTAAACCTTTTGGAAATGGAATTTGGAATCATCTAATGTGGAATGTCATTAG 300
DB 241 AAAAAAGTTAAACCTTTTGGAAATGGAATTTGGAATCATCTAATGTGGAATGTCATTAG 300

RESULT 2
AR176040
LOCUS AR176040
DEFINITION Sequence 18 from patent US 6310176.
ACCESSION AR176040
VERSION AR176040.1 GI:17917339
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 329)
Barra, D. and Simmaco, M.
TITLE Antimicrobially active polypeptides
JOURNAL Patent: US 6310176-A 18 30-OCT-2001;
FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.6e-65;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 GGAAGAGAGATGCCGATCGAAGAAAGAGAGATGATCTCGAAGAAAGGATGTTGAAGT 180
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DB 241 AAAAAAGTTAAACCTTTTGGAAATGGAATTTGGAATCATCTAATGTGGAATGTCATTAG 300

RESULT 3
BD268889
LOCUS BD268889
DEFINITION Transgenic plant having tolerance to wide-area pathogen.
ACCESSION BD268889
VERSION BD268889.1 GI:33078657
KEYWORDS JP 2002538828-A/2.
SOURCE Rana temporaria (common frog)
ORGANISM Rana temporaria
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana;
Rana.
REFERENCE
1 (bases 1 to 329)
Misra, S. and Kay, W.W.
AUTHORS Transgenic plant having tolerance to wide-area pathogen
TITLE Patent: JP 2002538828-A 2 19-NOV-2002;
JOURNAL UNIVERSITY OF VICTORIA INNOVATION AND DEVELOPMENT CORP
COMMENT OS Rana temporaria (european common frog)
PN JP 2002538828-A/2
PD 19-NOV-2002
PF 16-MAR-2000 JP 2000605754
PR 17-MAR-1999 US 60/125072
PI SANTOSH MISRA, WILLIAM W KAY
PC A01H5/00,C07K14/415/C12N5/10,C12N15/09,C12N15/00,C12N5/00 CC
Transgenic plant having tolerance to wide-area pathogen PH Key
LOCATION/Qualifiers
(53)..(235).
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Best Local Similarity 100.0%; Pred. No. 1.6e-65;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTCCAGCTGTCTACATCTCATTAACCACTGAACCCGAGCCCAAGATGTTTAC 60
DB 1 CCCCTCCAGCTGTCTACATCTCATTAACCACTGAACCCGAGCCCAAGATGTTTAC 60
QY 61 CTTGAAGAAATCCCTCTTACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 120
DB 61 CTTGAAGAAATCCCTCTTACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTG 120
QY 121 GGAAGAGAGATGCCGATCGAAGAAAGAGAGATGATCTCGAAGAAAGGATGTTGAAGT 180
DB 121 GGAAGAGAGATGCCGATCGAAGAAAGAGAGATGATCTCGAAGAAAGGATGTTGAAGT 180
QY 181 GGAAGAGAGATGTTTCCAGTGTGTTGGAAGGATCTCAATGGTATTTTGGGAAAATAAAC 240
DB 181 GGAAGAGAGATGTTTCCAGTGTGTTGGAAGGATCTCAATGGTATTTTGGGAAAATAAAC 240
QY 241 AAAAAAGTTAAACCTTTTGGAAATGGAATTTGGAATCATCTAATGTGGAATGTCATTAG 300
DB 241 AAAAAAGTTAAACCTTTTGGAAATGGAATTTGGAATCATCTAATGTGGAATGTCATTAG 300
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QY 301 CTAATGCGACATCAAAATGCTTTATAAAA 329
Db 301 CTAATGCGACATCAAAATGCTTTATAAAA 329

RESULT 4
LOCUS BD063212 329 bp DNA linear PAT 27-AUG-2002
DEFINITION Antimicrobially active polypeptides.
ACCESSION BD063212
VERSION BD063212.1 GI:22608815
KEYWORDS JP 2001506495-A/3.
SOURCE Rana temporaria (common frog)
ORGANISM Rana temporaria
REFERENCE 1 (bases 1 to 329)
AUTHORS Barra, D. and Simmaco, M.
TITLE Antimicrobially active polypeptides
JOURNAL Patent: JP 2001506495-A 3 22-MAY-2001;
COMMENT SBL VACCIN AB
OS Rana temporaria
PN JP 2001506495-A/3
PD 22-MAY-2001 JP 1998526559
PF 12-DEC-1997 JP 9604593-5
PI 13-DEC-1996 SE 9604593-5
PT DONNATELLA BARRA, MAURIZIO SIMMACO
PC C07K14/46, C07K7/08, A61K33/56
CC cDNA clone Rt-17
FH Key Location/Qualifiers
FT CDS (53)..(238)
FT mat peptide (191)..(229)
FT polyA signal (323)..(327)..
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ORIGIN
Query Match 100.0%; Score 329; DB 6; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.6e-65;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTCCAGCTGCTACATCTCATACCAACTGAACCCGAGCCCAAGATGTTAC 60
Db 1 CCCCTCCAGCTGCTACATCTCATACCAACTGAACCCGAGCCCAAGATGTTAC 60

QY 61 CTTGAAGAAATCCCTCTTACTCTCTTTCTCTTGGACATCAACTTATCTCTGTGA 120
Db 61 CTTGAAGAAATCCCTCTTACTCTTTCTCTTGGACATCAACTTATCTCTGTGA 120

QY 121 GGAAGAGAGATGCCGATCGAAGAGAGAGATGATCTCGAAGAGGATGTTGAAGT 180
Db 121 GGAAGAGAGATGCCGATCGAAGAGAGAGATGATCTCGAAGAGGATGTTGAAGT 180

QY 181 GGAAGAGAGATGTTTCCAGTGATTCGAAGGATACCTCAATGGTATTTTGGAAAAATAACC 240
Db 181 GGAAGAGAGATGTTTCCAGTGATTCGAAGGATACCTCAATGGTATTTTGGAAAAATAACC 240

QY 241 AAAAAAGTTAAACCTTTTGGAAATGGAATGGAATCATCTAATGTTGGAATGTCATTAG 300
Db 241 AAAAAAGTTAAACCTTTTGGAAATGGAATGGAATCATCTAATGTTGGAATGTCATTAG 300

QY 301 CTAATGCGACATCAAAATGCTTTATAAAA 329
Db 301 CTAATGCGACATCAAAATGCTTTATAAAA 329

LOCUS S69903 347 bp mRNA linear VRT 23-SEP-1994
DEFINITION Ranalexin=antimicrobial peptide polypeptide homolog [Rana
catesbeiana=bullfrog, metamorphic tadpoles, skin cells, mRNA, 347
nt].
ACCESSION S69903
VERSION S69903.1 GI:546211
KEYWORDS
SOURCE Rana catesbeiana (bullfrog)
ORGANISM Rana catesbeiana
REFERENCE 1 (bases 1 to 347)
AUTHORS Clark, D.P., Durell, S., Maloy, W.L. and Zasloff, M.
TITLE Ranalexin. A novel antimicrobial peptide from bullfrog (Rana
catesbeiana) skin, structurally related to the bacterial
antibiotic, polymyxin
JOURNAL J. Biol. Chem. 269 (14), 10849-10855 (1994)
MEDLINE 94193792
PUBMED 8144672
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsg 146812] from the original journal article.
FEATURES
Location/Qualifiers
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/organism="Rana catesbeiana"
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Method: conceptual translation with partial peptide
sequencing"
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/product="Ranalexin"
/protein_id="BAB30394.1"
/db_xref="GI:546212"
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KRFGLGLIKIVPAMICAVTKK"

ORIGIN
Query Match 66.2%; Score 217.8; DB 5; Length 347;
Best Local Similarity 84.8%; Pred. No. 6.4e-40;
Matches 279; Conservative 0; Mismatches 47; Indels 3; Gaps 3;

QY 3 CCTCCAGCTGTCTACATCTCATACCAACTGAACCCGAGCCCAAGATGTTACCT 62
Db 3 CTTCCAGCTGTCTACATCTCATACCAACTGAACCCGAGCCCAAGATGTTACCT 61

QY 63 TGAAGAAATCCCTCTTACTCTCTTTCTCTTGGACATCAACTTATCTCTGTGAGG 122
Db 62 TGAAGAAATCCCTGTGTACTCTCTTTCTCTTGGACATCAACTTATCTCTGTGAGG 121

QY 123 AAGAGAGATGCCGATCGAAGAGAGATGATCTCGAAGAGGATGTTGAAGTGG 182
Db 122 AAGAGAGAAATCCCGAAGAGAGAGAGATGATCTCGATGAAGGATGTTGAAGTGG 181

QY 183 AAAAGCGATTTTTCAGTGATTCGAAGGATACCTCAATGGTAT-TTTGGAAAAATAACCA 241
Db 182 AAAAGCGATTTTGGAGGCTTAATAAGATCGTTCAGCAATGATTTGTGAGTACCA 241

QY 242 AAAAAAGTTAAACCTTTTGGAAATGGAATCATCTAATGTTGGAATGTCATTAG 300
Db 242 AAAAAAGTTAAACCTTTTGGAAATGGAATCATCTAATGTTGGAATGTCATTAG 301

QY 301 CTAATGCGACATCAAAATGCTTTATAAAA 329
Db 302 CTAATATCACACCAGATGCTTTATAAAA 330

RESULT 6
S69903
RITTEMFORB

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LOCUS RTTEMPORB 323 bp mRNA linear VRT 02-OCT-2003
DEFINITION R.temporaria mRNA for temporin B precursor.
ACCESSION Y09393
VERSION Y09393.1 GI:1771589
KEYWORDS temporin B.
SOURCE Rana temporaria (common frog)
ORGANISM Rana temporaria
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana;
Rana.
REFERENCE 1
AUTHORS Simmaco,M., Mignogna,G., Canofeni,S., Miele,R., Mangoni,M.L. and Barra,D.
TITLE Temporins, antimicrobial peptides from the European red frog Rana temporaria
JOURNAL Eur. J. Biochem. 242 (3), 788-792 (1996)
MEDLINE 97175050
PUBMED 9022710
REFERENCE 2 (bases 1 to 323)
AUTHORS Barra,D.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1996) D. Barra, Universita La Sapienza, Dipartimento Di Scienze Biochimiche, Piazzale Aldo Moro 5, 00185 Roma, ITALY
FEATURES
source Location/Qualifiers
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/mol_type="mRNA"
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37..222
/function="antibacterial activity against gram-positive bacteria"
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/translation="MPTLKKSLLLFLFLGTLNLSLCEERNAEERRRDPDRDQVQE KRLLPVIGNLLKSLGK"
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/evidence=experimental
sig_peptide 37..103
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Query Match 64.7%; Score 212.8; DB 5; Length 323;
Best Local Similarity 83.4%; Pred. No. 9.1e-39;
Matches 257; Conservative 0; Mismatches 42; Indels 9; Gaps 1;
QY 22 TCATACCACTGAACCCGAGCCCAAGATGTTTCACCTTGAAGAAATCCCTCTTACT 81
DB 6 TCTGAGCCCACTGAACCCGAGCCCAAGATGTTTCACCTTGAAGAAATCCCTGTACT 65
QY 82 CCTTTTCTCTTGGGACCATCACTTATCTCTGTGAGGAAGAGAGATGCCGATGA 141
DB 66 CCTCTTTTCTTGGGACCATCACTTATCTCTGTGAGGAAGAGAGAAATGCAGA 125
QY 142 AGAAGAAGAGATGATCTCGAAGAAAGGATGTTGAAGTGGAAACGGATTTTCCAGT 201
DB 126 AGAAGAAGAGATGAACCAAGATGAAGGGATGTTCAAGTGGAAACCGACTTTTACCAAT 185
QY 202 GATTGGAAGTACTCAATGGTATTTTGGGAAATAACCAAAAGTTAAACTTTGGA 261
DB 186 TGTGGAACCTGCTCAAGAGCTTGTGGGAAATAACCA-----AAATGTTAAG 236
QY 262 AATGGAATTGGAATCATCTAATGTGGAATGTCATTTAGCTAAATGCACATCAATGTCT 321
DB 237 AATGGAATTGGAATCATCTGATGTGGAATATCAITTTAGCTAAATGCACATGTCT 296
QY 322 TATAAAAA 329
DB 297 TATTTAAA 304
RESULT 8
LOCUS BD063210
DEFINITION Antimicrobially active polypeptides.
ACCESSION BD063210
VERSION BD063210.1 GI:22608813
KEYWORDS JP 2001506495-A/1.
SOURCE Rana temporaria (common frog)
ORGANISM Rana temporaria
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana;
Rana.
REFERENCE 1 (bases 1 to 323)
AUTHORS Barra,D. and Simmaco,M.
TITLE Antimicrobially active polypeptides
JOURNAL Patent: JP 2001506495-A 1 22-MAY-2001;

Db 237 AATGGAATTGGAATCATCTGATGTGGAATATCAITTTAGCTAAATGCACATGTCT 296
QY 322 TATAAAAA 329
DB 297 TATTTAAA 304
RESULT 7
LOCUS ARL176038
DEFINITION Sequence 14 from patent US 6310176.
ACCESSION ARL176038
VERSION ARL176038.1 GI:17917337
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 323)
AUTHORS Barra,D. and Simmaco,M.
TITLE Antimicrobially active polypeptides
JOURNAL Patent: US 6310176-A 14 30-OCT-2001;
FEATURES
source Location/Qualifiers
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Query Match 64.7%; Score 212.8; DB 6; Length 323;
Best Local Similarity 83.4%; Pred. No. 9.1e-39;
Matches 257; Conservative 0; Mismatches 42; Indels 9; Gaps 1;
QY 22 TCATACCACTGAACCCGAGCCCAAGATGTTTCACCTTGAAGAAATCCCTCTTACT 81
DB 6 TCTGAGCCCACTGAACCCGAGCCCAAGATGTTTCACCTTGAAGAAATCCCTGTACT 65
QY 82 CCTTTTCTCTTGGGACCATCACTTATCTCTGTGAGGAAGAGAGATGCCGATGA 141
DB 66 CCTCTTTTCTTGGGACCATCACTTATCTCTGTGAGGAAGAGAGAAATGCAGA 125
QY 142 AGAAGAAGAGATGATCTCGAAGAAAGGATGTTGAAGTGGAAACGGATTTTCCAGT 201
DB 126 AGAAGAAGAGATGAACCAAGATGAAGGGATGTTCAAGTGGAAACCGACTTTTACCAAT 185
QY 202 GATTGGAAGTACTCAATGGTATTTTGGGAAATAACCAAAAGTTAAACTTTGGA 261
DB 186 TGTGGAACCTGCTCAAGAGCTTGTGGGAAATAACCA-----AAATGTTAAG 236
QY 262 AATGGAATTGGAATCATCTAATGTGGAATGTCATTTAGCTAAATGCACATCAATGTCT 321
DB 237 AATGGAATTGGAATCATCTGATGTGGAATATCAITTTAGCTAAATGCACATGTCT 296
QY 322 TATAAAAA 329
DB 297 TATTTAAA 304
RESULT 8
LOCUS BD063210
DEFINITION Antimicrobially active polypeptides.
ACCESSION BD063210
VERSION BD063210.1 GI:22608813
KEYWORDS JP 2001506495-A/1.
SOURCE Rana temporaria (common frog)
ORGANISM Rana temporaria
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana;
Rana.
REFERENCE 1 (bases 1 to 323)
AUTHORS Barra,D. and Simmaco,M.
TITLE Antimicrobially active polypeptides
JOURNAL Patent: JP 2001506495-A 1 22-MAY-2001;

SBL VACCIN AB
 OS Rana temporaria
 PN JP 2001506495-A/1
 PD 22-MAY-2001
 PF 12-DEC-1997 JP 1998526559
 PR 13-DEC-1996 SE 9604593-5
 PI DONNATELLA BARRA, MAURIZIO SIMMACO
 PC C07K14/46, C07K7/08, A61K33/56
 CC cDNA clone Rt-5
 FH Key
 FT CDS
 FT mat peptide
 FT polyA signal
 FT Location/Qualifiers
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Query Match 64.7%; Score 212.8; DB 6; Length 323;
 Best Local Similarity 83.4%; Pred. No. 9.1e-39;
 Matches 257; Conservative 0; Mismatches 42; Indels 9; Gaps 1;

QY 22 TCATACCACTGAACCCGAGCCCAAGATGTTACCTTGAGAAATCCCTCTTACT 81
 Db 6 TCTGAGCCCACTGAACCCGAGCCCAAGATGTTACCTTGAGAAATCCCTGTACT 65

QY 82 CTTTTTCTTCTGGGACCATCACTTATCTCTGTGAGGAAGAGAGATGCCGATCA 141
 Db 66 CTTCTTTTCTTGGGACCATCACTTATCTCTGTGAGGAAGAGAGAAATGCAGAGA 125

QY 142 AGAAGAAGAGATGATCTCGAAGAAAGGATGTTGAAGTGGAAACCGATTTTTTCCAGT 201
 Db 126 AGAAGAAGAGATGAACCAAGATGTTCAAGTGGAAACCGATTTTACCAGT 185

QY 202 GATTGGAAGTACTCAATGTTATTTTGGAAATTAACCAAAAGTTAAACTTTGA 261
 Db 186 TGTGGAAACCTGCTCAAGAGCTTGTGGAAATTAACCA-----AAATGTTAAG 236

QY 262 AATGGAATGGAAATCATTAATGTGGAATGTCATTTAGTAAATGCATCAATGTCT 321
 Db 237 AATGGAATGGAAATCATCTGATGTGGAATATCATTTAGTAAATGCATCAATGTCT 296

QY 322 TATAAAA 329
 Db 297 TATTAAA 304

RESULT 9
 RTEMPORH 356 bp mRNA linear VRT 02-OCT-2003
 LOCUS R. temporaria mRNA for temporin H precursor.
 DEFINITION Y09394
 ACCESSION Y09394
 VERSION Y09394.1 GI:1771593
 KEYWORDS temporin H.
 SOURCE Rana temporaria (common frog)
 ORGANISM Rana temporaria
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana;
 Rana.

REFERENCE 1
 AUTHORS Simmaco, M., Mignogna, G., Canofeni, S., Miele, R., Mangoni, M.L. and Barra, D.
 TITLE Temporins, antimicrobial peptides from the European red frog Rana temporaria
 JOURNAL Eur. J. Biochem. 242 (3), 788-792 (1996)
 MEDLINE 97175050
 PUBMED 9022710
 REFERENCE 2 (bases 1 to 356)
 AUTHORS Barra, D.
 TITLE Direct Submission
 JOURNAL Submitted (11-NOV-1996) D. Barra, Universita La Sapienza,

Dipartimento Di Scienze Biochimiche, Piazzale Aldo Moro 5, 00185 Roma, ITALY
 FEATURES source
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ORIGIN
 Query Match 61.9%; Score 203.8; DB 5; Length 356;
 Best Local Similarity 81.7%; Pred. No. 1.1e-36;
 Matches 267; Conservative 0; Mismatches 42; Indels 18; Gaps 2;

QY 3 CTTCCAGCTGTCTACATCTCTATAACCACTGAACCCGAGCCCAAGATGTTACCT 62
 Db 29 CTTCCAGCGTCTACATCTCTGAGCACCACCTGACTACCCGAGCCCAAGATGTTACCT 88

QY 63 TGAAGAAATCCCTTTACTCTCTTTCTTCTTGGGACCATCAACTATCTCTCTGTGAGG 122
 Db 89 TGAAGAAATCCCTGTTACTCTCTCTTTCTTCTTGGGACCATCAACTATCTCTCTGTGAGG 148

QY 123 AAGAGAGAGATGCCCATGAAGAAAGAGATGATCTCGAAGAAAGGGATGTTGAAGTGG 162
 Db 149 AAGAGAGAAATCCGAGAAAGAAAGAGATGAACCATGAAGGGATGTTCAAGTGG 208

QY 183 AAAAGCGATTTTCTCCAGTGATGGAAGGATCACTCAATGGTATTTTGGGAAATACCAA 242
 Db 209 AAAAGCGATTTTCTCC-----AACTCTCAAGAGCTTGTGGGAAATACCAA- 258

QY 243 AAAAGTTTAAACTTTGGAATGGAATGGAATCATCTTAATGTGGAATGTCATTTAGCT 302
 Db 259 -----AAAATGTTAAGATGGAATGGAATCATCTGATGTGGAATATCATTTAGCT 310

QY 303 AAATGCATCAATGCTCTTATAAAA 329
 Db 311 AAATGCCAACAGATGCTTATTAAA 337

RESULT 10
 AR176039 356 bp DNA linear PAT 17-DEC-2001
 LOCUS Sequence 16 from patent US 6310176.
 DEFINITION AR176039
 ACCESSION AR176039
 VERSION AR176039.1 GI:17917338
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 356)
 AUTHORS Barra, D. and Simmaco, M.
 TITLE Antimicrobially active polypeptides
 JOURNAL Patent: US 6310176-A 16 30-OCT-2001;
 FEATURES Location/Qualifiers

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source          1. .356
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Query Match          61.9%; Score 203.8; DB 6; Length 356;
Best Local Similarity 81.7%; Pred. No. 1.1e-36;
Matches 267; Conservative 0; Mismatches 42; Indels 18; Gaps 2;

QY 3 CTCCAGCTGTCTACATTCTCATACCAACTGAACCCCGAGCCCAAGAGATGTTTCACCT 62
DB 29 CTTCCAGCGTCTACATTCTGAGCACCACCTGAAGATCTCCGAGCCCAAGAGATGTTTCACCT 88

QY 63 TGAAGAAATCCCTCTTACTCTCTTTCTTCTTGGGACCACTCAACTTATCTCTCTGTGAGG 122
DB 89 TGAAGAAATCCCTGTACTCTCTTTCTTCTTGGGACCACTCAACTTATCTCTCTGTGAGG 148

QY 123 AAGAGAGAGTCCCGATGAGAGAAAGAGATGATCTCGAAGAAAGGGATGTTGAAGTGG 182
DB 149 AAGAGAGAAATGCAAGAAGAAAGAGATGAACCAAGATGAAGGGGATGTTCAAGTGG 208

QY 183 AAAACGGATTTTTCAGTGATTTGAAGGATCTCAATGGTATTTTGGGAAATTAACCAA 242
DB 209 AAAACGACTTTCACCTCTTTCTTCTTGGGACCACTCAACTTATCTCTCTGTGAGG 148

QY 123 AAGAGAGAGTCCCGATGAGAGAAAGAGATGATCTCGAAGAAAGGGATGTTGAAGTGG 182
DB 149 AAGAGAGAAATGCAAGAAGAAAGAGATGAACCAAGATGAAGGGGATGTTCAAGTGG 208

QY 183 AAAACGGATTTTTCAGTGATTTGAAGGATCTCAATGGTATTTTGGGAAATTAACCAA 242
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QY 243 AAAAGTTTAAACTTTGGAATGGAATGGAATGGAATCATCTAATCTGGAATGTCATTTAGCT 302
DB 259 -----AAAATGTTAAGATGGAATGGAATCATCTGATGTGGAATATCATTTAGCT 310

QY 303 AAATGCACATCAATGCTCTTATAAAA 329
DB 311 AAATGCCAACAGATGCTCTATTATAA 337

RESULT 12
REBRELE
LOCUS          R.esculenta mRNA for brevinin-1E.          363 bp          linear          VRT 19-JUN-1996
DEFINITION
ACCESSION      X77831
VERSION        X77831.1 GI:488372
KEYWORDS       brevinin.
SOURCE         Rana esculenta (edible frog)
ORGANISM       Rana esculenta
               Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana;
               Pelophylax.

REFERENCE
AUTHORS        Simmaco, M., Mignogna, G., Barra, D. and Bossa, F.
TITLE          Antimicrobial peptides from skin secretions of Rana esculenta.
JOURNAL        Molecular cloning of cDNAs encoding esculentin and brevinins and
MEDLINE        Isolation of new active peptides
PUBMED         J. Biol. Chem. 269 (16), 11956-11961 (1994)
               94216303
               8163497

REFERENCE
AUTHORS        Simmaco, M.
TITLE          Direct Submission
JOURNAL        Submitted (10-FEB-1994) M. Simmaco, Nodo Nazionale Italiano (area
               di, ricerca CNR-Bari), Via Amendola 168/5, 70126 Bari, ITALY

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               /db_xref="UniProt/Swiss-Prot:P32412"
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ORIGIN
Query Match          59.5%; Score 195.8; DB 5; Length 363;
Best Local Similarity 81.7%; Pred. No. 1.1e-36;
Matches 267; Conservative 0; Mismatches 42; Indels 18; Gaps 2;

source          1. .356
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ORIGIN
Query Match          61.9%; Score 203.8; DB 6; Length 356;
Best Local Similarity 81.7%; Pred. No. 1.1e-36;
Matches 267; Conservative 0; Mismatches 42; Indels 18; Gaps 2;

QY 3 CTCCAGCTGTCTACATTCTCATACCAACTGAACCCCGAGCCCAAGAGATGTTTCACCT 62
DB 29 CTTCCAGCGTCTACATTCTGAGCACCACCTGAAGATCTCCGAGCCCAAGAGATGTTTCACCT 88

QY 63 TGAAGAAATCCCTCTTACTCTCTTTCTTCTTGGGACCACTCAACTTATCTCTCTGTGAGG 122
DB 89 TGAAGAAATCCCTGTACTCTCTTTCTTCTTGGGACCACTCAACTTATCTCTCTGTGAGG 148

QY 123 AAGAGAGAGTCCCGATGAGAGAAAGAGATGATCTCGAAGAAAGGGATGTTGAAGTGG 182
DB 149 AAGAGAGAAATGCAAGAAGAAAGAGATGAACCAAGATGAAGGGGATGTTCAAGTGG 208

QY 183 AAAACGGATTTTTCAGTGATTTGAAGGATCTCAATGGTATTTTGGGAAATTAACCAA 242
DB 209 AAAACGACTTTCACCTCTTTCTTCTTGGGACCACTCAACTTATCTCTCTGTGAGG 148

QY 123 AAGAGAGAGTCCCGATGAGAGAAAGAGATGATCTCGAAGAAAGGGATGTTGAAGTGG 182
DB 149 AAGAGAGAAATGCAAGAAGAAAGAGATGAACCAAGATGAAGGGGATGTTCAAGTGG 208

QY 183 AAAACGGATTTTTCAGTGATTTGAAGGATCTCAATGGTATTTTGGGAAATTAACCAA 242
DB 209 AAAACGACTTTCACCTCTTTCTTCTTGGGACCACTCAACTTATCTCTCTGTGAGG 148

QY 243 AAAAGTTTAAACTTTGGAATGGAATGGAATGGAATCATCTAATCTGGAATGTCATTTAGCT 302
DB 259 -----AAAATGTTAAGATGGAATGGAATCATCTGATGTGGAATATCATTTAGCT 310

QY 303 AAATGCACATCAATGCTCTTATAAAA 329
DB 311 AAATGCCAACAGATGCTCTATTATAA 337

RESULT 11
BD063211
LOCUS          Antimicrobially active polypeptides.          356 bp          DNA          linear          PAT 27-AUG-2002
DEFINITION
ACCESSION      BD063211
VERSION        BD063211.1 GI:22608814
KEYWORDS       Rana temporaria (common frog)
SOURCE         Rana temporaria
ORGANISM       Rana
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana;
               Rana.

REFERENCE
AUTHORS        Barra, D. and Simmaco, M.
TITLE          Antimicrobially active polypeptides
JOURNAL        Patent: JP 2001506495-A 2 22-MAY-2001;
               SBL VACCIN AB

COMMENT
OS             Rana temporaria
PN             JP 2001506495-A/2
PD             22-MAY-2001
PF             12-DEC-1997 JP 1998526559
PR             13-DEC-1996 SE 9604593-5
PI             DONNATELLA BARRA, MAURIZIO SIMMACO
PC             C07K14/46,C07K7/08,A61K33/56
CC             cDNA clone Rt-6
FH             Key
FT             CDS
FT             Location/Qualifiers
FT             (79) . (255)
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FT             (217) . (246)
FT             polyA_signal
FT             (307) . (311) .
               Location/Qualifiers
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ORIGIN
Query Match          61.9%; Score 203.8; DB 6; Length 356;
Best Local Similarity 81.7%; Pred. No. 1.1e-36;
Matches 267; Conservative 0; Mismatches 42; Indels 18; Gaps 2;

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Matches	270;	Conservative	0; Mismatches 57; Indels 10; Gaps 3;
QY	3	CTCTCCAGCTGTCTACATTCTCATAAACCAACTGAACCAACCCAGAGCCCAAGAGTGTTCACCT	62
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QY	63	TGAAGAAATCCCTCTTACTCTCTTTCTTCTTTGGAGCCATCAACTTATCTCTCTGTGAGG	122
Db	67	TGAAGAAATCAATGTTTACTCTCTTTCTTCTTTGGAGCCATCAACTTATCTCTCTGTGAGG	126
QY	123	AAGAGAGAGATGCCGAT---GAAGAAAGAGAGATGATCTCGAAGAAGGGATGCTTCAAG	179
Db	127	AAGAGAGATGCCGATGGAAGAAGAAGAGAGACAATCCAGATGAAGAAGTGAAGTTCGAAG	186
QY	180	TGGAAGAGCGATTTTTTCCAGTGATTTGGAAGGATACCTCAATGGTGATTTTGGGAAAA---	235
Db	187	TGGAAGAACGATTTCTTCCATTGTTGGCAGTCTGGCTGCTAAATTTCTTGCCGAAGATAT	246
QY	236	TAACCAAAAAAGTTAAAAACTTTTGGAAA---TGGAATTGGAATATCATCTAATGTGGAATG	292
Db	247	TTTGTAATAATAACCAAGAAATGTTTGAACCTTTTGAAATTGGAAATCACTGTATGTGGAAAA	306
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158. .229
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ORIGIN

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Best Local Similarity 76.6%; Pred. No. 7.5e-28;		
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Db	9	ACCAACTGAACACTACCAAGAACCCAAAGATGTTCACCTTGAAGAAATCCCTGTACTCCTTT 68
Qy	87	TCCTTCCTTGGGACCATCAACTTATCTCTCTGTGAGNAGAGAGAGATGCCGATGAAGAAA 146
Db	69	TCCTTCCTTGGGACCATCAGCTTATCTCTCTGTGAGGAAGAGAGAAATGCCCGATGAAGAAG 128
Qy	147	GAAGAGATGATCTCGAAGAAAGGGATGTTGAACTGGAAAGCGATTTTTTCCAGTGAATTG 206
Db	129	AAAAAAGAGATGTGAAG--TGAAAAACGATTTTTTGGGGAGCACTCTTCAAGGTGGCTTC 186
Qy	207	GAAGGATACTCAATGGTATTTTGGGAAAAATAACCAAAAAAAGTTAAACCTTTGGAAATGG 266
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Qy	267	AATTGGAAATCATCTAATGTGGAATCTCATTTAGCTTAAATGCACATCAAAATGCTTTATAA 326
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Qy	327	AAA 329
Db	299	AAA 301

RESULT	14
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LOCUS	RPI427746 linear VRT 12-MAR-2003
DEFINITION	Rana pipiens mRNA for brevinin 1pb.
ACCESSION	AJ427746
VERSION	AJ427746.1 GI:20145828
KEYWORDS	antimicrobial peptide; brevinin 1pb.
SOURCE	rana pipiens (northern leopard frog)
ORGANISM	Rana pipiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana;
	Pantherana.
REFERENCE	1
AUTHORS	Chen,T., Farragher,S., Bjourson,A.J., Orr,D.F., Rao,P. and Shaw,C.
TITLE	Granular gland transcriptsomes in stimulated amphibian skin secretions
JOURNAL	J. Biochem. 371, 125-130 (2003)
REFERENCE	2 (bases 1 to 294)
AUTHORS	Farragher,S.M.
TITLE	Direct Submission
JOURNAL	Submitted (10-JAN-2002) Farragher S.M., School of Biomedical Sciences, University of Ulster, Cromore Road, N. Ireland., UNITED KINGDOM

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ORIGIN

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Best Local Similarity 76.8%; Pred. No. 3.2e-24;
Matches 216; Conservative 0; Mismatches 49; Indels 17; Gaps 2;

QY 53 ATGTTACCTTGAAGAAATCCCTCTTACTCTCTTTCTTCTTCTGGGACCATCAACTTATCT 112
DB 4 ATGTTACCTTGAATAAATCTCTTCTTCTTCTTCTTCTTCTGGGACCATCAACTTATCT 63

QY 113 CTCTGTGAGAGAGAGAGATGCCGATGAAGAAAGAGAGATCTCGAAGAAAGGAT 172
DB 64 TTCTGTGAGAGAGAGAGATGAAGAAAGAGAGATGAGCCAGATGAAGACGAT 120

QY 173 GTTGAAGTGAAGAGGATTTTTCAGATGATTGGAGGATA-----CTCA 218
DB 121 GTTGAAGTGAAGAGGATTTTTCAGATGATTGGAGGATGAGCCAGATGAGTCTTCCCG 180

QY 219 ATGCTATTTTGGGAAATTAACCAAAAAAGTTAAAACTTTGGAATGGAATGGAATCA 278
DB 181 AAAATATTTGTCATATAGCAAAAAATGTTGAACTTTGGAACCTTTGGAATGGAATCA 240

QY 279 TCTAATGTGAATGTCTATTAGCTAATGACATCAAAATGTC 320
DB 241 TCTGATGAGATATCATTTAGCTAATGACATCAAAATGTC 282

RESULT 15

RP1414584
LOCUS Rana pipiens mRNA for peptide leucine arginine precursor (pLR).
DEFINITION
ACCESSION AJ414584
VERSION AJ414584.1 GI:15990856
KEYWORDS peptide leucine arginine precursor.
SOURCE Rana pipiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana; Pantherana.

REFERENCE 1
Farragher, S., Bjourson, A.J., McClean, S., Orr, D.F. and Shaw, C.
Cloning of cDNAs encoding defensive skin secretion peptides from the Northern leopard frog (Rana pipiens)
Unpublished
REFERENCE 2 (bases 1 to 362)
Farragher, S.
Direct Submission
Submitted (17-SEP-2001) Farragher S., School of Biomedical Sciences, University of Ulster, Cromore Road, Coleraine, Northern Ireland, BT52 1SA, UNITED KINGDOM
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Best Local Similarity 64.8%; Pred. No. 1.2e-18;
Matches 212; Conservative 0; Mismatches 96; Indels 19; Gaps 1;

QY 3 CCTCCAGCTGTCTACATTTCTCATAAACCAACTGAATACCCGAGCCCAAGATGTTCACT 62
DB 19 CTTCCAGTTGTCTCATTTCTCAGCACCACCACTGAATACCCGAGCCCAAGATGTTCACT 78

QY 63 TGAAGAAATCCCTCTTACTCTCTTCTTCTTCTGGGACCATCAACTTATCTCTCTGAGG 122
DB 79 TGAAGAAATCCCTGTGTTACTCTTCTTCTTCTTCTGGGACCATCTCTCTCTGTGAGC 138

QY 123 AAGAGAGAGATGCCGATGAAGAAAGAGAGATCTCGAAGAAAGGATGTTGAAGTGG 182
DB 139 AAGAGAGAGATGCCGATGATGAAGATCAAGGGGAAAGTTACAGAACAAAGTTGTAATA 194

QY 183 AAAAGCGATTTTTCAGCTGATTGGAAGGATCACTCAATGGTATTTTGGGAAATTAACCAA 242
DB 195 -----AGATTAGTCAGAGGGTCTCGACCAAGAGTTATCCCAAGGCT 239

QY 243 AAAAGTTTAAACTTTTGGAAATGGAATGGAATCATCTAATGTGGAATGTCATTTAGCT 302
DB 240 TGTGTTGTAAGAGGATAAACATGAATTTGGAAGTCACTGATGTGGAATATCATTTGGCT 299

QY 303 AAATGCACATCAAAATGCTTTATAAAAA 329
DB 300 AAATGCTAAATGCTGTGATAAAAAATAA 326

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Job time : 1392 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 14:38:32 ; Search time 256 Seconds

(without alignments)
7607.793 Million cell updates/sec

Title: US-10-719-623a-15

Perfect score: 329

Sequence: 1 cccctccagctgtctacatt.....catcaaatgtcttataaaaa 329

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseqn1980b:*
- 3: Geneseqn2000a:*
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- 5: Geneseqn2001a:*
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- 9: Geneseqn2003a:*
- 10: Geneseqn2003b:*
- 11: Geneseqn2003cs:*
- 12: Geneseqn2004a:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	329	100.0	329	3	AAV75750 cDNA enco
3	212.8	64.7	323	2	AAV07447 Rana temp
4	203.8	61.9	356	2	AAV07448 Rana temp
5	46.8	14.2	341	13	ADR8892 Nucleotid
6	45	13.7	443	3	AAV75749 cDNA enco
7	40.6	12.3	403	6	ABN77187 Human ORF
8	40.2	12.2	414	10	ADC30694 Human nov
9	40.2	12.2	4804	5	ABV30199 Human pro
10	40	12.2	56153	4	AAS46794 Tumour su
11	39.4	12.0	8781	6	ABL33686 Human imm
12	39.2	11.9	64976	2	AAV21209 16
13	38.6	11.7	466	4	AAI36639 Probe: #53
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16	38.6	11.7	23934	4	AAU36171 Human mus
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21	38.6	11.7	23934	5	ABA19145 Human ner
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28	38.4	11.7	14950	6	ABL33257 Human imm
29	38	11.6	765	6	ABK80955 Bacillus
30	38	11.6	220860	12	ADN36595 Human pro
31	37.8	11.5	5852	2	AAQ11710 Dictyoste
32	37.8	11.5	177866	10	ADL13935 Osteoarth
33	37.4	11.4	747	3	AAC38796 Arabidops
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35	37	11.2	300	5	AAS88161 DNA enco
36	37	11.2	436	6	ABL37759 Human col
37	37	11.2	3502	4	ABL07145 Drosophil
38	37	11.2	8152	4	ABL07144 Drosophil
39	37	11.2	17738	6	ABL33538 Human imm
40	36.8	11.2	402	5	AA875450 DNA enco
41	36.8	11.2	600	2	AAV86185 EST clone
42	36.8	11.2	1176	2	AAV66903 Canine he
43	36.8	11.2	1176	4	AAF26723 Canine he
44	36.8	11.2	5495	2	AAAT75590 Canine he
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ALIGNMENTS

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DT 26-OCT-1998 (first entry)
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DE Rana temporaria temporin G cDNA.
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KW Tempoin G; anti-microbial property; anti-fungal property; ss.
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XX
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FT /tag= c
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XX WO9825961-A1.
XX
XX 18-JUN-1998.
XX
XX 12-DEC-1997; 97WO-SB002075.
XX
XX 13-DEC-1996; 96SE-00004593.
XX
XX (SBLV-) SBL VACCIN AB.
XX Barra.D, Simmaco M;
XX WPI; 1998-362423/31.
XX P-PSDB; AAW51843.
XX
XX Peptides from the skin of the frog Rana temporaria - useful as anti-microbial or anti-fungal compositions.


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XX 18-JUN-1998.
XX 12-DEC-1997; 97WO-SE002075.
XX 13-DEC-1996; 96SE-00004593.
XX (SBLV-) SBL VACCIN AB.
XX Barra D, Simmaco M;
XX WPI; 1998-362423/31.
XX P-PSDB; AAW51841.
XX Peptides from the skin of the frog Rana temporaria - useful as anti-
PT microbial or anti-fungal compositions.
XX Claim 11; Page 18; 27pp; English.
XX The present sequence represents the Rana temporaria temporin B cDNA
CC isolated from a R. temporaria skin cDNA library. The cDNA encodes a
CC temporin B peptide which has anti-microbial properties. The invention
CC claims for other R. temporaria derived peptides which are claimed to be
CC useful in medicaments for anti-microbial and anti-fungal use
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Best Local Similarity 83.4%; Pred. No. 2.6e-48;
Matches 257; Conservative 0; Mismatches 42; Indels 9; Gaps 1;

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DB 6 TCTGAGCCCACTGACACCCGAGCCCAAGAGTGTTCACCTTCAAGAAATCCCTCTTACT 65
QY 82 CTTTTCCTTCCTGGGACCATCAACTTATCTCTGTGAGGAAGAGAGATCCCGATGA 141
DB 66 CCTCTTTTCTTGGGACCATCAACTTATCTCTGTGAGGAAGAGAGAAATGCAAGA 125
QY 142 AGAAGAAGAGATGATCTCAAGAAAGAGTGTGAGTGGAAAGCGGATTTTCCAGT 201
DB 126 AGAAGAAGAGATGATCAAGAAAGAGTGTGAGTGGAAAGCGGATTTTACCAAT 185
QY 202 GATTGGAAGGATCTCAATGGTATTTTGGGAAATTAACCAAAAGTTAAATTTTGA 261
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QY 322 TATAAAA 329
DB 297 TATTTAAA 304

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XX
XX 26-OCT-1998 (first entry)
XX
XX Rana temporaria temporin B cDNA.
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XX Temporin H; anti-microbial property; anti-fungal property; ss.
XX
XX Rana temporaria.

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FT /*tag= b
FT mat_peptide 217..246
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XX WO9825961-A1.
XX Barra D, Simmaco M;
XX 18-JUN-1998.
XX 12-DEC-1997; 97WO-SE002075.
XX 13-DEC-1996; 96SE-00004593.
XX (SBLV-) SBL VACCIN AB.
XX Barra D, Simmaco M;
XX WPI; 1998-362423/31.
XX P-PSDB; AAW51842.
XX Peptides from the skin of the frog Rana temporaria - useful as anti-
PT microbial or anti-fungal compositions.
XX Claim 11; Page 18; 27pp; English.
XX The present sequence represents the Rana temporaria temporin H cDNA
CC isolated from a R. temporaria skin cDNA library. The cDNA encodes a
CC temporin H peptide which has anti-microbial properties. The invention
CC claims for other R. temporaria derived peptides which are claimed to be
CC useful in medicaments for anti-microbial and anti-fungal use
XX
XX Sequence 356 BP; 124 A; 69 C; 72 G; 91 T; 0 U; 0 Other;

Query Match 61.9%; Score 203.8; DB 2; Length 356;
Best Local Similarity 81.7%; Pred. No. 7.8e-46;
Matches 267; Conservative 0; Mismatches 42; Indels 18; Gaps 2;

QY 3 CTCCAGCTGTCTACATTTCTATCAACCAACTGAACCAACCCGAGCCCAAGAGATGTTCACT 62
DB 29 CTTCCAGCGTCTACATTTCTGAGCACCACCAACTGAACCTACCCGAGCCCAAGAGATGTTCACT 88
QY 63 TGAAGAAATCCCTCTTACTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 122
DB 89 TGAAGAAATCCCTCTTACTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 148
QY 123 AAGAGAGAGATCCGATGAAGAAAGAGAGATGATCTCGAAGAAAGAGGATGTTGAAGTGG 182
DB 149 AAGAGAGAAATCGAAGAAAGAGAGAGATGATGACCAATGAAGAGGATGTTCAAGTGG 208
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DB 209 AAAAGCGATTTTTCAGTGTGGAAGGATCTCAATGATTTTGGGAAATAAACCA- 258
QY 243 AAAAGGTTAAACTTTGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 302
DB 259 -----AAAATGTTAAGATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 310
QY 303 AAATGCACATCAATCTCTTATAAAA 329
DB 311 AAATGCGCAACAGATGTTTATTTAAA 337

RESULT 5
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ID ADR88892 standard; cDNA; 341 BP.
XX
XX ADR88892;

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XX	19-NOV-2004	(first entry)
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XX	DE	Nucleotide sequence of tryptophyllin-1 designated Pdt-1.
XX	KW	tryptophyllin-1; pdt-1; vasodilatory; frog; defensive skin secretion;
XX	KW	vasodilation; ischaemic heart disease; ischaemic disease;
XX	KW	vascular stenosis; occlusion; hypertension; blood-brain barrier;
XX	KW	anti-cancer; angiogenesis; healing; disease; transplant; graft;
XX	KW	spinal cord injury; cardiovascular disease; arterial smooth muscle;
XX	KW	central nervous system disorder; infection; inflammation; cancer; tumour;
XX	KW	Hodgkin's disease; non-Hodgkin's lymphoma; multiple myeloma;
XX	KW	haematopoietic malignancy; glaucoma; pulmonary hypertension; stroke;
XX	KW	atherosclerosis; asthma; ophthalmologic disease; renal failure;
XX	KW	menstrual disorder; obstetric condition; wound; gastrointestinal disease;
XX	KW	anaphylactic shock; endotoxic shock; ss.
XX	OS	Pachymedusa dactinicolor.
XX	XX	
XX	Key	Location/Qualifiers
XX	CDS	55..243
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XX	PD	02-SEP-2004.
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XX	PF	04-FEB-2004; 2004WO-IB000806.
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XX	PR	05-FEB-2003; 2003GB-00002621.
XX	PR	06-JUN-2003; 2003GB-00012990.
XX	XX	
XX	PA	(UYUL-) UNIV ULSTER.
XX	PA	(SHAW/) SHAW C.
XX	PA	(HIRS/) HIRST D.
XX	PA	(CHEN/) CHEN T.
XX	PA	(OROU/) O'ROURKE M.
XX	XX	
XX	PI	Shaw C, Hirst D, Chen T, O'roucke M;
XX	DR	
XX	WPI	2004-642491/62.
XX	DR	P-PSDB; ADR88893.
XX	XX	
XX	PT	Isolated tryptophyllin peptide obtained from biologically active analog
XX	PT	of Pachymedusa dactinolor tryptophyllin-1, having vasodilatory activity,
XX	PT	useful for treating conditions of vascular insufficiency e.g., ischemic
XX	PT	heart disease.
XX	XX	
XX	PS	Claim 49; SEQ ID NO 17; 55pp; English.
XX	XX	
XX	CC	The present sequence encodes a full length tryptophyllin-1, derived from
XX	CC	Pachymedusa dactinolor and designated Pdt-1. The specification describes
XX	CC	tryptophyllin-1 peptides and Pdt-1 analogues which have a vasodilatory
XX	CC	activity. Tryptophyllin-1 peptides are isolated from frog defensive skin
XX	CC	secretions. Tryptophyllin-1 peptides of the invention are useful for
XX	CC	preparing a medicament for treating disorders where vasodilation is
XX	CC	beneficial, such as ischaemic heart disease, ischaemic disease of other
XX	CC	organs or organ systems, vascular stenoses, occlusion to peripheral
XX	CC	vessels, or hypertension, and for increasing the transport of
XX	CC	biologically active compounds across the blood-brain barrier, where the
XX	CC	biologically active compound is an anti-cancer drug. They are useful for
XX	CC	promoting angiogenesis, for treating conditions of vascular
XX	CC	insufficiency, to promote healing at sites of transplantation and
XX	CC	grafting, and for treating spinal cord injuries. They are also useful for
XX	CC	treating cardiovascular disease, for increasing vasodilation, for
XX	CC	treating hypertension, for dilating arterial smooth muscle. In
XX	CC	combination with other therapeutic agents, peptides of the invention are
XX	CC	useful for treating disorders in the brain including central nervous

CC	system disorder, bacterial, viral and fungal infections, inflammation and
CC	cancer, tumour, Hodgkin's disease, non-Hodgkin's lymphomas, multiple
CC	myeloma and haematopoietic malignancies. Tryptophyllin-1 peptides of the
CC	invention are also useful in treating glaucoma, pulmonary hypertension,
CC	stroke, atherosclerosis, asthma, ophthalmologic disease, renal failure,
CC	menstrual disorder, obstetric conditions, wound, gastroenteric disease,
CC	anaphylactic or endotoxic shock, etc. .
XX	
QQ	Sequence 341 BP; 132 A; 55 C; 74 G; 80 T; 0 U; 0 Other;
	Query Match 14.2%; Score 46.8; DB 13; Length 341;
	Best Local Similarity 60.0%; Pred No. 0.0089;
	Matches 78; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
QY	44 AGCCCAAGATGTTTCACCTTGAAGAAATCCCTCTTACTCCTTTTCTCTCTGGGACCATC 103
DB	46 AGACCAATATGAATTTCTTGAAGAAGTCGCTTTTCTTGCTGTTCTCTCGGATTCGT 105
QY	104 AACTTATCTCTGTGTAGGAAGAGAGATGCCGATGAGAAAGAGAGATGATCTCGAA 163
DB	106 TCCATTTCCTTCTGTGTATGAAGAGAAACAGGATGACGATGAGGGGAATGAGAGAGAG 165
QY	164 GAAAGGGATG 173
DB	166 GAAAGAAAG 175
RESULT 6	
AAA75749	
ID	AAA75749 standard; cDNA; 443 BP.
XX	
AC	AAA75749;
XX	
DT	22-JAN-2001 (first entry)
XX	
DE	cDNA encoding a dermaseptin precursor polypeptide.
XX	
XX	Dermaseptin; antibacterial; fungal growth; temporin; transgenic plant;
KW	cationic peptide; pathogen resistance; ss.
KW	
XX	
OS	Phyllomedusa bicolor.
XX	
FH	Key Location/Qualifiers
FT	CDS 58..294
FT	/*tag= a
FT	/product= "dermaseptin"
XX	
PN	WO200055337-A1.
XX	
PD	21-SEP-2000.
XX	
PF	16-MAR-2000; 2000WO-CR000288.
XX	
PR	17-MAR-1999; 99US-0125072P.
XX	
PA	(UVVI-) UNIV VICTORIA INNOVATION & DEV CORP.
XX	
PI	Misra S, Kay WD;
XX	
XX	WPI; 2000-647077/62.
DR	P-PSDE; AAB18724.
DR	
PT	Transgenic plants resistant to broad spectrum of pathogens useful for
PT	producing biologically active cationic peptides, comprises nucleic acid
FT	molecule encoding temporin and/or dermaseptin peptides.
XX	
XX	Disclosure; Page 46; 58pp; English.
XX	
CC	The present sequence encodes a dermaseptin precursor polypeptide. The
CC	precursor is processed to produce two mature forms, dermaseptin b
CC	(AAB18725) and dermaseptin B (AAB18726). Dermaseptin has antibacterial
CC	activity, and inhibits fungal growth. Cationic peptides derived from
CC	temporins and dermaseptins are used to produce transgenic plants. The

transgenic plants are useful for producing biologically active cationic peptides such as temporins and dermaseptins in large quantities. The CC peptide confers broad spectrum pathogen resistance including enhanced CC resistance to both fungal and bacterial pathogens in the transgenic CC plants. The transgenic plants may be used in conventional agricultural CC applications such as food crops, medical and other applications

XX
SQ Sequence 443 BP; 211 A; 60 C; 77 G; 95 T; 0 U; 0 Other;

Query Match 13.7%; Score 45; DB 3; Length 443;
Best Local Similarity 65.3%; Pred. No. 0.03;
Matches 66; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy 44 AGCCCAAGATGTTACCTTGAAGAATAATCCTCTTACTTCCTTTCTCTCGTGGAACCATC 103
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 49 AGAACAAACATGGATATCCTCGAAGAAATCTCTTTTCTGTATTATTCTTGATGTTGTT 108
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 104 AACTTATCTCTCTGTGAGGAGAGAGATGCCGATGAAGA 144
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 109 TCCCTTTCCATCTGTGAAGAGAAAAGAAAAATGAAGA 149
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
ABN77187/c
ID ABN77187 standard; cDNA; 403 BP.
XX
AC ABN77187;
XX
DT 08-JUL-2002 (first entry)
XX
DE Human ORF2134 cDNA, SEQ ID NO:4267.
XX
KW Human; ORF; open reading frame; ORFX; drug screening; diagnosis;
KW disease monitoring; cytokine; cell proliferation; cell differentiation;
KW immune modulation; haematopoiesis regulation; tissue growth;
KW angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
KW behaviour; cancer; proliferative disorder; neurological disorder;
KW cardiovascular disease; immune system disorder; organ transplantation;
KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
KW hypothyroidism; cholesterol ester storage disease; infection; vulnery;
KW vasotropic; antipsoriatic; antidiabetic; cytostatic; neurotropic;
KW neuroprotective; antiatherosclerotic; anticoagulant; thrombolytic;
KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
KW dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.

OS Homo sapiens.
XX
PN W0200190366-A2.
XX
PD 29-NOV-2001.
XX
PF 24-MAY-2001; 2001WO-US017076.
XX
PR 24-MAY-2000; 2000US-0206690P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Leach MD, Shimkets RA;
XX
DR WPI; 2002-106209/14.
XX
DR P-PSDB; ABP33161.
XX
PT Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and disorders related to organ
transplantation.
XX
PS Claim 1; Page 1323; 2508pp; English.
XX
CC Sequences ABP31028-ABP35561 represent 4534 novel human proteins
CC designated ORF (open reading frame) 1-4534, and sequences ABN75054-
CC ABN79587 represent cDNAs encoding them. The invention also encompasses

	polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX polynucleotides and polypeptides, methods of screening for modulators of ORFX expression or activity, and methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, haematopoiesis regulation, tissue growth, angiogenesis, activin or inhibin activity, chemotactic/chemokinetic activity, haemostatic activity, thrombolytic activity, receptor/ligand, anti-inflammatory activity, tumour inhibition activity, and antitensive activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, nucleic acids and antibodies may be used in the treatment of cancers, other proliferative disorders such as psoriasis and benign tumours, neurological disorders such as epilepsy and Alzheimer's disease, cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. ORFX nucleic acids may also be used as a source of primers and probes, in the detection of ORFX genomic sequences or transcripts, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The ORFX nucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases
XX	
SQ	Sequence 403 BP; 106 A; 71 C; 73 G; 153 T; 0 U; 0 Other;
	Query Match 12.3%; Score 40.6; DB 6; Length 403; Best Local Similarity 51.4%; Pred. No. 0.47; Matches 94; Conservative 0; Mismatches 89; Indels 0; Gaps 0
OY	144 AAAGAAGATGATCTCGAAGAAAGGATGTGAAGTGGAAAACGCATTTTTCACAGTA 203 DB 293 ATACNAATGATCAGTAGCATATCTATGCTCATGTGAAGCAACTTTTTTCTCAGCTT 234
OY	204 TTGGAAGGATCTCAATGGTGATTTTGGGAAAAATAACCAAAAAGTTTAAACCTTTGGAAA 263
DB	233 TAGTAAAAATATTCTTAGATTTTTTGAAGAAGATAAAGCATTTAAATAATTAGTAGTAGA 174
OY	264 TGGNATGGGAATCATCTATATGGAATGTCTTTAGCTAAATGCCACATCAAATGTCTTA 323
DB	173 CAACACGCTACATGAGCTATAGAAATATGGCATATTTCTCAATGGACATAGAATGCTTCA 114
OY	324 TAA 326
DB	113 TCA 111
RESULT 8	
ADC30694	ID ADC30694 standard; cDNA; 4414 BP.
XX	ADC30694;
AC	
XX	
DT	18-DEC-2003 (first entry)
XX	
DE	Human novel cDNA sequence, SEQ ID NO:776.
XX	
KW	Human; diagnostic; drug screening; forensics; gene mapping;
KW	biodiversity assessment; Parkinson's disease; Alzheimer's disease;
KW	neurodegenerative diseases; anaemia; platelet disorder; wound; burns;
KW	ulcers; osteoporosis; autoimmune disease; cancer;
KW	molecular weight marker; food supplement; antiparkinsonian; nootropic;
KW	neuroprotective; anti-anemic; anticoagulant; thrombolytic; vulnery;
KW	antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostatic;
KW	kne therapy; chromosome 1; gene; ss.

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XX OS Homo sapiens.
XX PN WO2003029271-A2.
XX PD 10-APR-2003.
XX PF 24-SEP-2002; 2002WO-US030474.
XX PR 24-SEP-2001; 2001US-0324631P.
XX PA (HYSB-) HYSQ INC.
XX PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
PI Zhou F, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
PI Haley-Vicente D, Drmanac RT;
XX DR WPI; 2003-371981/35.
XX DR P-PSDB; ADC31665.
XX PT New polynucleotide and polypeptide useful for diagnosing, preventing or
PT treating conditions such as neurodegenerative diseases, anemias, platelet
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT cancer.
XX PS Claim 1; SEQ ID NO 776; 1185pp; English.
XX CC The invention relates to 971 novel human cDNA sequences (ADC29919-
CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of preventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human cDNA sequence of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 4414 BP; 1497 A; 828 C; 1167 G; 922 T; 0 U; 0 Other;

Query Match 12.2%; Score 40.2; DB 10; Length 4414;
Best Local Similarity 54.4%; Pred. No. 1.5;
Matches 81; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 120 AGGAAGAGAGATGCCGATGAAGAAGAGAGATGATCTCGAAGAAAGGATTTTCAAG 179
DB AGGTATAGAAAGAAGAGAAAGAGAGAGAACTAGAGGAAGAGAGAGAGAGAGAGG 2279
QY 180 TGGAAAAAGCGATTTTTTCCAGTGATTTGGAAGGATCTCAATGGTATTTTGGGAAATAAC 239
DB AGGAAGAAGAAAGGAATCAGGAGACTGCAGAAATTCCTTCTTAGTAGTAGTAAGAAATAGAAA 2339

XX OS Homo sapiens.
XX PN WO2003029271-A2.
XX PD 10-APR-2003.
XX PF 24-SEP-2002; 2002WO-US030474.
XX PR 24-SEP-2001; 2001US-0324631P.
XX PA (HYSB-) HYSQ INC.
XX PI Tang TY, Zhang J, Ren F, Xue AJ, Zhao QA, Wang J, Wehrman T;
PI Zhou F, Ghosh M, Wang D, Ma Y, Asundi V, Wang Z, Weng G;
PI Haley-Vicente D, Drmanac RT;
XX DR WPI; 2003-371981/35.
XX DR P-PSDB; ADC31665.
XX PT New polynucleotide and polypeptide useful for diagnosing, preventing or
PT treating conditions such as neurodegenerative diseases, anemias, platelet
PT disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
PT cancer.
XX PS Claim 1; SEQ ID NO 776; 1185pp; English.
XX CC The invention relates to 971 novel human cDNA sequences (ADC29919-
CC ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The
CC invention also relates to nucleic acid sequences over 99% identical with
CC the novel human cDNAs. The invention additionally encompasses expression
CC vectors and host cells comprising a nucleic acid of the invention; the
CC recombinant production of a polypeptide of the invention; an antibody
CC against a polypeptide of the invention; a method of detecting
CC polynucleotides or polypeptides of the invention; and methods of
CC identifying a compound which binds to a polypeptide of the invention. The
CC invention further discloses methods of preventing, treating or
CC ameliorating a medical condition; kits comprising polynucleotide probes
CC and/or monoclonal antibodies for carrying out the methods of the
CC invention; methods for the identification of compounds that modulate the
CC expression or activity of the polynucleotide and/or polypeptide; and 767
CC contig sequences corresponding to the cDNA sequences of the invention
CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628
CC -ADC33394). The nucleic acids and polypeptides of the invention are
CC useful in diagnostics, drug screening, forensics, gene mapping, in the
CC identification of mutations responsible for genetic disorders or other
CC traits, for assessing biodiversity, and in producing many other types of
CC data and products dependent on DNA and amino acid sequences. They are
CC also used for treating diseases such as Parkinson's disease, Alzheimer's
CC disease and other neurodegenerative diseases, anemia, platelet
CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
CC cancer. The nucleic acids may also be used as hybridisation probes or
CC primers, and in the recombinant production of a protein. The polypeptides
CC are also useful in generating antibodies, as molecular weight markers,
CC and as food supplements. The present sequence represents a specifically
CC claimed human cDNA sequence of the invention. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 4414 BP; 1497 A; 828 C; 1167 G; 922 T; 0 U; 0 Other;

Query Match 12.2%; Score 40.2; DB 10; Length 4414;
Best Local Similarity 54.4%; Pred. No. 1.5;
Matches 81; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 120 AGGAAGAGAGATGCCGATGAAGAAGAGAGATGATCTCGAAGAAAGGATTTTCAAG 179
DB AGGTATAGAAAGAAGAGAAAGAGAGAGAACTAGAGGAAGAGAGAGAGAGAGG 2279
QY 180 TGGAAAAAGCGATTTTTTCCAGTGATTTGGAAGGATCTCAATGGTATTTTGGGAAATAAC 239
DB AGGAAGAAGAAAGGAATCAGGAGACTGCAGAAATTCCTTCTTAGTAGTAGTAAGAAATAGAAA 2339
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QY 240 CAAAAAAGCTTAAACTTTGGAAATGGAA 268
DB 2340 CAAAAGATGAAAAGAAATGGATAAGAA 2368

RESULT 9
ABV30199
ID ABV30199 standard; cDNA; 4804 BP.
XX AC ABV30199;
XX DT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 30190.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX PN WO200160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US005171.
XX PR 17-FEB-2000; 2000US-0183319P.
XX PR 16-MAR-2000; 2000US-0189862P.
XX PR 25-MAY-2000; 2000US-0207454P.
XX PR 09-JUN-2000; 2000US-0211314P.
XX PR 18-JUL-2000; 2000US-0219007P.
XX PR 13-DEC-2000; 2000US-0255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer.
XX PS Claim 1; Page 6542-6543; 11750pp; English.
XX CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for: (a) assessing whether
CC a patient is afflicted with prostate cancer; (b) monitoring the
CC progression of prostate cancer in a patient; (c) assessing the efficacy
CC of a test compound to inhibit prostate cancer in a patient; (d) assessing
CC the efficacy of a therapy for inhibiting prostate cancer in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound; (g)
CC determining whether prostate cancer has metastasized in a patient; (h)
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC assessing the aggressiveness or indolence of prostate cancer in a patient
CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker
XX SQ Sequence 4804 BP; 1605 A; 910 C; 1244 G; 1016 T; 0 U; 29 Other;

Query Match 12.2%; Score 40.2; DB 5; Length 4804;
Best Local Similarity 54.4%; Pred. No. 1.5;
Matches 81; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 120 AGGAAGAGAGATGCCGATGAAGAAGAGAGATGATCTCGAAGAAAGGATTTTCAAG 179
DB AGGTATAGAAAGAAGAGAAAGAGAGAGAACTAGAGGAAGAGAGAGAGAGAGG 2133
QY 180 TGGAAAAAGCGATTTTTTCCAGTGATTTGGAAGGATCTCAATGGTATTTTGGGAAATAAC 239
DB AGGAAGAAGAAAGGAATCAGGAGACTGCAGAAATTCCTTCTTAGTAGTAGTAAGAAATAGAAA 2193
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Query Match	12.2%	Score 40;	DB 4;	Length 56153;
Matches	91;	Conservative	Mismatches	86;
Matches	91;	Conservative	Mismatches	0;
gaps	0;	indels	gaps	0;

